

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:21:38 ; Search time 17 Seconds
(without alignments)
891.319 Million cell updates/sec

Title: US-09-936-845A-15
Perfect score: 1545
Sequence: 1 MELAEFNDLNTFTYGNPH.....PFVKAYIIKSKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1545	100.0	291	1	YLPA_CABEL	Q03574 caenorhabdi
2	564	36.5	435	1	YYS_CABEL	P49191 caenorhabdi
3	492	31.8	270	1	ELO3_HUMAN	Q9H803 homo sapien
4	479	31.0	271	1	ELO3_MOUSE	Q35949 mus musculu
5	263.5	17.1	312	1	ELO4_MOUSE	Q9EGC4 mus musculu
6	262	17.0	345	1	ELO3_YEAST	P40319 saccharomyc
7	261	16.9	314	1	ELO4_MACFA	Q9SK73 macaca fasc
8	254	16.4	314	1	ELO4_HUMAN	Q9GXR5 homo sapien
9	239.5	15.5	279	1	ELO1_MOUSE	Q9JJJ5 mus musculu
10	239	15.5	279	1	ELO1_HUMAN	Q9BW60 homo sapien
11	220.5	14.3	310	1	ELO1_YEAST	P39540 saccharomyc
12	220	14.2	347	1	ELO2_YEAST	P25358 saccharomyc
13	219	14.2	282	1	ELO2_MOUSE	Q9JJJ4 mus musculu
14	214	13.9	286	1	ELO2_HUMAN	Q9NB29 homo sapien
15	102	6.6	880	1	YE21_ARCFU	O28851 archaeoglob
16	99.5	6.4	919	1	YKQ5_YEAST	P36051 saccharomyc
17	97.5	6.3	498	1	TLCA_RICPR	P19568 rickettsia
18	96.5	6.2	392	1	OLSF_DROME	Q9VHE6 drosophila
19	96	6.2	473	1	NOR8_PSEST	P98008 pseudomonas
20	95	6.1	359	1	E124_HUMAN	O14681 homo sapien
21	93	6.1	2671	1	IP3T_HUMAN	Q14573 homo sapien
22	93.5	6.1	759	1	NAHS_ONCMY	Q01345 oncornynchu
23	92	6.0	526	1	ALG8_HUMAN	Q9BWK7 homo sapien
24	91.5	5.9	289	1	Y771_ARCFU	O29487 archaeoglob
25	91.5	5.9	317	1	O6N2_HUMAN	Q8NGY6 homo sapien
26	91.5	5.9	503	1	ALG6_CABEL	Q09226 caenorhabdi
27	91.5	5.9	629	1	CTR1_HUMAN	P30825 homo sapien
28	91	5.9	591	1	FZD9_HUMAN	O00144 homo sapien
29	91	5.9	873	1	SYA_WIGER	Q8DW88 wigleswort
30	90.5	5.9	466	1	NOR6_PSEAE	O59647 pseudomonas
31	90	5.8	466	1	GAC2_RAT	P18508 rattus norv
32	90	5.8	474	1	GAC2_MOUSE	P22723 mus musculu
33	89.5	5.8	295	1	LPLC_BACSU	P39129 bacillus su

34	89.5	5.8	308	1	AMID_STRPN	P18794 streptococc
35	89	5.8	474	1	GAC2_CHICK	P21548 gallus gall
36	89	5.8	621	1	P2L2_MOUSE	Q9J194 mus musculu
37	89	5.8	1564	1	PDR2_YEAST	P51533 saccharomyc
38	88.5	5.7	246	1	CAH_XLEPN	O52535 klebsiella
39	88.5	5.7	532	1	COXI_RHOCA	P98059 rhodobacter
40	88	5.7	358	1	E124_MOUSE	Q61070 mus musculu
41	88	5.7	405	1	DITB_LACRH	P35855 lactobacill
42	88	5.7	467	1	GAC2_HUMAN	P18507 homo sapien
43	87	5.6	590	1	YKTA_CABEL	P34322 caenorhabdi
44	86	5.6	236	1	Y147_RICPR	Q92E15 rickettsia
45	86	5.6	451	1	GNTF_ZYMWMO	Q92670 zymomonas m

ALIGNMENTS

RESULT 1

YLPA_CABEL
ID YLPA_CABEL STANDARD; PRT; 291 AA.

AC Q03574;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 34.1 kDa protein C40H1.4 in chromosome III.

GN C40H1.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson K., Ainscough R., Anderson K., Baynes C., Berks M., Cooper J., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R., Sims M., Smallon N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
RL Nature 368:32-38(1994)
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the ELO family.

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CC EMBL; Z19154; CAA79555.1; -
CC PIR; S28299; S28299.
DR WormPep; C40H1.4; CE00112.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 254 274 POTENTIAL.
SQ SEQUENCE 291 AA; 34059 MW; 6657272A53B343F CRC64;

Query Match 100.0%; Score 1545; DB 1; length 291;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAEFNDLNTFYGNPTDMTKYKYSVHPGEQVADPOYWTILFQKYWHSITISV 60
 DB 1 MELAEFNDLNTFYGNPTDMTKYKYSVHPGEQVADPOYWTILFQKYWHSITISV 60
 QY 61 LYFILLIKVQKFMENRKPFTLKYPILLWNGALAAFSIIATLRSIDPLSLYAGFPYKTL 120
 DB 61 LYFILLIKVQKFMENRKPFTLKYPILLWNGALAAFSIIATLRSIDPLSLYAGFPYKTL 120
 QY 121 CYSNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIFLHYHHAANLIYTVHSGAEH 180
 DB 121 CYSNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIFLHYHHAANLIYTVHSGAEH 180
 QY 181 TAAGREFIILNYPFAHSLMYTYTVTSANGYRLPKWVSMVTVTQTTOMLAGVGITWVYKV 240
 DB 181 TAAGREFIILNYPFAHSLMYTYTVTSANGYRLPKWVSMVTVTQTTOMLAGVGITWVYKV 240
 QY 241 KTEYKLPQCOQSVANLYLAFVIYVTFALLFQFPVKAYIIKSSKSKSVQNE 291
 DB 241 KTEYKLPQCOQSVANLYLAFVIYVTFALLFQFPVKAYIIKSSKSKSVQNE 291

RESULT 2
 YFS3_CABEL STANDARD; PRT; 435 AA.
 AC P49191;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
 GN D2024.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du Z., Gattung S.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the ELO family.
 CC
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 CC
 CC EMBL; U41011; AAA82288.1; -;
 DR PIR; T34200; T34200.
 DR WormPep; D2024.3; CE04292.
 DR InterPro; IPR002076; GNS1_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 SQ SEQUENCE 435 AA; 5148 MW; F7940A74A1969914 CRC64;

Query Match 36.5%; Score 564; DB 1; Length 435;
 Best Local Similarity 42.0%; Pred No. 1.4e-39;
 Matches 128; Conservative 45; Mismatches 56; Indels 46; Gaps 7;

QY 22 DMTTKY---KYSVHPGEQVADPOYWTILFQKYWHSITISVFIILI-----KVI----- 69
 DB 5 DYNPKYGLENYISILFPETSPDPRSTWQNHVQISITASVYVAVIFGKKVLIYKK 64

QY 70 -----QKF--MENRKPFTLKYPILLWNGALAAFSIIATLUR 102
 DB 65 SRVITPESSLOAKNENKSLNSSQFOMEKYPFOLDTFLFVWNSFLAIFSLGFLR 124
 QY 103 FSIDPLRSIYAGS--FYKTLCYSCNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIP 160
 DB 125 MTEPEFVWSAGSNGSFKYSICHSSYAQGVGTGWTFQFAMSKLFLDITIFIVLRKPLIP 184
 QY 161 LHYHHAANLIYTVHSGAEHTAAGRFYIILNYPFAHSLMYTYTVTSANGYRLPKWVSMVTVT 220
 DB 185 LKWHYHVTVMYTVTHAYKDHDTASGRFIMWYGVHVALMYSYVALRSKLPKQAMAVVT 244
 QY 221 TVQTTOMLAGVGITWVYKVT--EYKLPQCOQSVANLYLAFVIYVTFALLFQFPVKAYI 278
 DB 245 TLQLAQMGMVGIIGTVTVIRKSGY---CQQTWDNLGFCFGYFYFILLPANFFYHAYV 301
 QY 279 IKSSK 283
 DB 302 KKNR 306

RESULT 3
 ELO3_HUMAN STANDARD; PRT; 270 AA.
 ID ELO3_HUMAN
 AC Q9H803; Q8N180;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Elongation of very long chain fatty acids protein 3 (Cold inducible
 DE glycoprotein of 30 kDa).
 GN ELOVL3 OR CIG30.
 DE ELOVL3 OR CIG30.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RC MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buesow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McWhan P.J., McKernan K.J., Abramson R.D., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.F., Skalska U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 35-270 FROM N.A.
 RA Semina E.V., Murray J.C.;
 RA "The CIG30/PITX3/GDF1 gene configuration is conserved between human
 RA and mouse genomes."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May be involved in a membrane event related to cellular
 CC proliferation in brown adipose tissue. Could be implicated in
 CC synthesis of very long chain fatty acids and sphingolipids. May
 CC catalyze one or both of the reduction reaction in fatty acid
 CC elongation, i.e., conversion of beta-ketoacyl CoA to beta-
 CC hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated
 CC acyl CoA derivative (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

RA MEDLINE=94299524; PubMed=8027068;
RA Garcia-Arreaza M., Maldonado A.M., Mazon M.J., Portillo F.;
RT "Transcriptional control of yeast plasma membrane H(+)-ATPase by
RT glucose. Cloning and characterization of a new gene involved in this
RT regulation.";
RN J. Biol. Chem. 269:18076-18082(1994).
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnson M., Hillier L., Riles L., Albermann K., Andre B., Ansoorge W.,
RA Barnes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA Etian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger P., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moesl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=99054745; PubMed=9832547;
RA David D., Sundarababu S., Gerst J.E.;
RT "Involvement of long chain fatty acid elongation in the trafficking of
RT secretory vesicles in yeast.";
RL J. Cell Biol. 143:1167-1182(1998).
RN [6]
RN CHARACTERIZATION.
RX MEDLINE=97362220; PubMed=9211877;
RA Oh C.-S., Toke D.A., Mandala S., Martin C.E.;
RT "ELO2 and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene,
RT function in fatty acid elongation and are required for sphingolipid
RT formation.";
RL J. Biol. Chem. 272:17376-17384(1997).
CC -!- FUNCTION: Affects plasma membrane H+-ATPase activity. May act on a
CC glucose-signaling pathway that controls the expression of several
CC genes that are transcriptionally regulated by glucose such as
CC PMAL1, HXT3 and SNF3. Could be also a component of the membrane
CC bound fatty acid elongation systems that produce the 26-carbon
CC very long chain fatty acids that are precursors for ceramide and
CC sphingolipids. Is essential for the conversion of 24-carbon fatty
CC acids to 26 carbon species.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the ELO family.
CC -----
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CC -----
DR EMBL; L28723; AAA35134.1; -
DR EMBL; X82033; CAAS7553.1; -
DR EMBL; X78326; CAAS5129.1; -
DR EMBL; U19103; AAB67563.1; -
DR EMBL; AF011409; AAC28398.1; -
DR PIR; S48517; S48517.
DR GERMOnline; 142436; -
DR SGD; S0004364; SUR4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IDA.
DR GO; GO:0009922; P:fatty acid elongase activity; IMP.
DR GO; GO:0030497; P:fatty acid elongation; IMP.
DR GO; GO:0006892; P:post-Golgi transport; IGI.
DR GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.

KW Fatty acid biosynthesis; Transmembrane.
PT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 284 304 POTENTIAL.
FT CONFLICT 35 35 E -> D (IN REF. 3).
FT CONFLICT 208 208 W -> R (IN REF. 3).
FT CONFLICT 330 331 ST -> FY (IN REF. 3).
SQ SEQUENCE 345 AA; 39465 MW; 130A9ACS4BFCCS CRC64;

Query Match 17.0%; Score 262; DB 1; Length 345;
Best Local Similarity 28.9%; Pred. No. 1.2e-14;
Matches 82; Conservative 53; Mismatches 115; Indels 34; Gaps 11;

QY 27 YKSYHFCEQVADQYWTILFQKQWYHSITSLVLYLKIYQKME--NEKPTFLKYP 84
DB 50 FYFSGYFAEQFEFHINKTEFLAN--GYHVSIIIVYIIIFGQAILRLNASPLKFKLL 107
QY 85 LILWNGALAAFSIIATLRFSDPLSLYAEQFYKTLG--YSCNPTDVAAFWSFAPALSKI 142
DB 108 FEIHNLFSTISLVLMLEQLVPMVYHNGLFWSICKEAFAPKLVTLY--VLNVLTKF 165
QY 143 VELGDTMFIILKRPLILHYHH--AAVLIVTSHGAEHTAAGRFYILMNYFAHSLMYT 200
DB 166 VELIDTVFLVLRKLLFLHTYHGGATALLCYQLIG--RTSVVWVILLINLGVHVTW 223
QY 201 YTVSGAMGYRFPKVMVMTVTVTQTTMLAGVITWMVYKVKTEY-----KLPCQ 249
DB 224 VYFLSSCGIRV--WVKQWTRFQIIQFL--IDLVFVYFATYFYAHKYLDGILPNKGTCTY 279
QY 250 QSVANLYLAFVYVTFPAILTQFPFKVYIIKSKK--SKSVKNE 291
DB 280 GTQAAAYGYLILFTSYLLLFISFYIQSY-----KXGKRTVKKE 318

RESULT 7
ELO4 MACFA STANDARD; PRT; 314 AA.
ID ELO4 MACFA
AC Q95K73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation of very long chain fatty acids 4 protein.
GN ELOVL4
OS Eukarya fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]_TaxID=9541;
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=22651545; PubMed=12806887;
RA Umeda S., Ayyagari R., Suzuki M.T., Ono F., Iwata F., Fujiki K.,
RA Kanai A., Takada Y., Yoshikawa Y., Tanaka Y., Iwata T.;
RT "Molecular cloning of ELOVL4 gene from cynomolgus monkey (Macaca
RT fascicularis)." ;
RT Exp. Anim. 52:129-135(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Temporal cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries." ;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the biosynthesis of very long chain fatty
CC acids. Seems to represent a photoreceptor-specific component of
CC the fatty acid elongation system residing on the endoplasmic
CC reticulum.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -!- TISSUE SPECIFICITY: Expressed mainly in retina. Also expressed in

CC skin and thymus.
CC -1- SIMILARITY: Belongs to the ELO family.
CC -----
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CC -----
CC EMBL: AF461182; AAC015594.1; -
CC DR EMBL: AF461187; AAC015601.1; -
CC DR EMBL: AF461183; AAC015601.1; JOINED.
CC DR EMBL: AF461184; AAC015601.1; JOINED.
CC DR EMBL: AF461185; AAC015601.1; JOINED.
CC DR EMBL: AF461186; AAC015601.1; JOINED.
CC DR EMBL: AB063100; BAB60806.1; -
CC DR InterPro: IPR002076; GNS1_SUR4.
CC DR Pfam: PF01151; ELO_1.
CC DR PROSITE: PS01188; ELO_1.
CC KW Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
CC FT TRANSMEM 42 62 POTENTIAL.
CC FT TRANSMEM 78 98 POTENTIAL.
CC FT TRANSMEM 165 185 POTENTIAL.
CC FT TRANSMEM 188 208 POTENTIAL.
CC FT TRANSMEM 247 267 POTENTIAL.
CC FT SITE 310 312 ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
CC FT (POTENTIAL).
CC FT CARBOHYD 20 20 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT SEQUENCE 314 AA; 36812 MW; 560FE00C91D96766 CRC64;
CC -----
CC Query Match 16.9%; Score 261; DB 1; Length 314;
CC Best Local Similarity 30.3%; Pred. No. 1.3e-14;
CC Matches 87; Conservative 57; Mismatches 97; Indels 46; Gaps 19;
CC -----
CC Qy 22 DMITKYKSYHFFQEQVADQYWTILPQKYHYSITISVLYFLIKVIOKFMENRKEFTL 81
CC Db 21 DTVEFYRWTSIADKRV---ENNP-LMQSPW-PTLSISTLLFLVFMGPKMKNDREPFQM 75
CC -----
CC Qy 82 KYPLILWNGALAPSIITLRFSDPLRSIYAEQF---YKTLG---YSCNPIDV---A 130
CC Db 76 RLVLIIYN-----FGV-LNFFI--FRELFGSYNAGSYVICSDVSNVNEVRLAA 127
CC -----
CC Qy 131 AFWSFALSKIVELGDMTFILKR--PLIFLHYTHAAVLIVTV-HSGAETHAQR-- 185
CC Db 128 LMYWF---VSKGVEYLDVTPFLAKQNNQVSLFHVHCT--MFTLWIGIKWVAGQQA 182
CC -----
CC Qy 186 FYILMNYFAHSLMYTVTSAMGYRLPK--WVSMVTVTVTOTMLAGVITWVYKVKTE 243
CC Db 183 FGAQNSFIHVMISYGLAAGFPWIKYLNKKYLTMLQLVQPHVTHGT--ALSLYTD 240
CC -----
CC Qy 244 YKLPQOSVANLYLAFVIY-VTFALFQPFVKAAYIIKSKKSXVK 289
CC Db 241 CPEP-----KWHWALIAVAFISFPLFLNFYRTY--KEPKKPTGK 280
CC -----
CC RESULT 8
CC ELO4 HUMAN
CC ID ELO4 HUMAN STANDARD; PRT; 314 AA.
CC AC Q9GZRS; Q86YJ1; Q9H139;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Elongation of very long chain fatty acids protein 4.
CC GN ELOV14.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A., AND VARIANT VAL-299.
CC TISSUE=Retina;

RX MEDLINE=20578755; PubMed=11138005;
RA Zhang K., Kniazeva M., Han M., Li W., Yu Z., Yang Z., Li Y.,
RA Metzker M.B., Allikmets R., Zack D.J., Kakuk L.E., Lagali P.S.,
RA Wong P.W., McDonald I.M., Sieving P.A., Figueroa D.J., Austin C.P.,
RA Gould R.J., Ayyagari R., Petrukhin K.;
RT "A 5-bp deletion in ELOV14 is associated with two related forms of
RT autosomal dominant macular dystrophy.";
RL Nat. Genet. 27:89-93 (2001).
RN [2].
RP SEQUENCE FROM N.A.
RX MEDLINE=21464738; PubMed=11581213;
RA Edwards A.O., Donoso L.A., Ritter R. III;
RT "A novel gene for autosomal dominant Stargardt-like macular dystrophy
RT with homology to the SUR4 protein family.";
RL Invest. Ophthalmol. Vis. Sci. 42:2652-2663 (2001).
RN [3].
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma N., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4].
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932;
RA Klausner R.L., Fellngold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Prange C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5].
RP SEQUENCE OF 35-314 FROM N.A.
RA Dunn M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6].
RP VARIANTS THR-267 and VAL-299.
RX MEDLINE=22480060; PubMed=12592226;
RA Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
RT "Evaluation of the ELOV14 gene in patients with autosomal recessive
RT retinitis pigmentosa and Leber congenital amaurosis.";
RL Mol. Vision 9:49-51 (2003).
CC -1- FUNCTION: Involved in the biosynthesis of very long chain fatty
CC acids. Seems to represent a photoreceptor-specific component of
CC the fatty acid elongation system residing on the endoplasmic
CC reticulum. May be implicated in docosahexaenoic acid (DHA)
CC biosynthesis, which requires dietary consumption of the essential
CC alpha-linolenic acid and a subsequent series of three elongation
CC steps. May be involved in one of these three elongation steps.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in the retina and at much lower

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Could be implicated in tissue-specific synthesis of very
CC long chain fatty acids and sphingolipids. May catalyze one or both
CC of the reduction reaction in fatty acid elongation, i.e.,
CC conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
CC reduction of trans-2-enoyl CoA to the saturated acyl CoA
CC derivative.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (potential).
CC -!- TISSUE SPECIFICITY: Expressed in a broad variety of tissues.
CC Highly expressed in stomach, lung, kidney, skin and intestine.
CC Moderately expressed in white adipose tissue, liver, spleen,
CC brain, brown adipose tissue, heart and muscle. Weakly expressed in
CC testis.
CC -!- SIMILARITY: Belongs to the ELO family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF170907; AAF72572.1; -;
CC EMBL; BC006735; AAH06735.1; -;
CC EMBL; AK003743; BAB22975.1; -;
CC MGD; MGI:1858959; Elov11.
CC InterPro; IPR002076; GNS1_SUR4.
CC Pfam; PF0151; ELO; 1.
CC PROSITE; PS01188; ELO; 1.
CC Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
CC TRANSMEM 23 43
CC TRANSMEM 61 81
CC TRANSMEM 176 196
CC TRANSMEM 203 223
CC TRANSMEM 231 251
CC SITE 275 277
CC
CC CONFLICT 78 79
CC SEQUENCE 279 AA; 32678 MW; CASA1CF55FDB2F76 CRC64;
CC
CC Query Match 15.5%; Score 239.5; DB 1; Length 279;
CC Best Local Similarity 28.6%; Pred. No. 6.8e-13;
CC Matches 78; Conservative 51; Mismatches 101; Indels 43; Gaps 13;
CC
CC QY 39 ADP--QYWTILPKQYWHISITISLVLYFLIKVIQFMENRKPFTLYKPLILWNGALAAFS 96
CC DQ 15 ADPRIQSYPLMGSPILLITSLITLVYVFFIL-SIGPRIMANRPFQRLRGFMIVNFSVLVS 73
CC QY 97 ITATURFSDIDPRLSYAGFYKTYLCYCNPTD-----VAAPFAPFALSIVELG 146
CC DQ 74 LVIVYEFLLM-----SGWLSTYTWRCDDIDFNSPEALRMVRVAV--LPLMSKVIELM 123
CC QY 147 DTPMFLIRKES--PLIFLHYVHAALVLYTVHSGAHT--AAGRFYILMNYPAHSLMYTTY 202
CC DQ 124 DVIIFILRKQKQVTFLLVAFH-SVLPWSWVWGIKIAQGWGSGFAMINSVHVWLYLY 182
CC QY 203 TVSANGYRLP-----KWSMVTYVTVQTO-MIAGVITVMYKTYEKLPCQGSVANLY 256
CC DQ 183 GLSALG---PVAQPVLMKKHMTAQILQFVLVSLHSIYYFMPSCNYQP-----LIH 234
CC QY 257 LAFVIYVTFAILFIQFVKAYIKSKSKSVK 289
CC DQ 235 LIWYGTPIFLPSFWHSHY-TKGRLPRAVQ 266

RESULT 10
ELO1_HUMAN

ID ELO1_HUMAN STANDARD; PRT; 279 AA.
AC Q9BWM0; Q9NVD9; Q9Y396;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation of very long chain fatty acids protein 1 (CGI-88).
GN ELOVLI OR SSC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20272150; PubMed=10810093;
RA Lai C.-H., Chou C.-Y., Chang L.-Y., Lin C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masubo Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Could be implicated in tissue-specific synthesis of very
CC long chain fatty acids and sphingolipids. May catalyze one or both
CC of the reduction reaction in fatty acid elongation, i.e.,
CC conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
CC reduction of trans-2-enoyl CoA to the saturated acyl CoA
CC derivative (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (potential).
CC -!- SIMILARITY: Belongs to the ELO family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 189.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF151846; AAD34083.1; ALT_FRAME.
CC EMBL; AK001653; BAA91813.1; -;
CC EMBL; BC000618; AAH00618.1; -;

QY 144 ELGDTMFIILRKPLI-----FLHY-----YHRAVLI 171
Db 154 -IGSLIAALLISLATAAFAYMYAFRWVKSLEEFKEIFPGSGEMHFSALLPASFLLSAALI 212
QY 172 Y-----TVHSGAEH-TAAGRFYILANNYPFAHSLMYTYTYSAMGYRLPKWVSMTVTVTQTT 225
Db 213 YLSRFEIVHS--EHGLISGASIVDWNILSPSLMF-----LSAI 248
QY 226 QMLAGVGITWVYKVKTEYKLPQQOSVANLYLAFVIYVTFAILPFIQFFKAYIIKSKKS 285
Db 249 VLLSGGIFAAYIVARRRVERVF---QIVGVLFVIALLLTFV---APFFVQKFWVPSLS 301

Search completed: June 16, 2004, 15:28:01
Job time : 18 secs

Db 260 KPMKDMQEPAGKEVKN 277
RESULT 15
YE21_ARCFU STANDARD; PRT; 880 AA.
AC O28851;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0182 protein AF1421.
GN AF1421.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
3N
2P SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.B.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Foucherry B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Sadger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0182 family.

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EXEL; AE001005; AAB89825.1; --
DR FIR; D69427; D69427.
DR TIGR; AF1421; --
DR HAKAP; MF_01600; -- 1.
DR InterPro; IPR005372; UPF0182.
DR Pfam; PF03699; UPF0182; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 19 41 POTENTIAL.
FT TRANSMEM 61 83 POTENTIAL.
FT TRANSMEM 103 125 POTENTIAL.
FT TRANSMEM 152 174 POTENTIAL.
FT TRANSMEM 195 217 POTENTIAL.
FT TRANSMEM 237 259 POTENTIAL.
FT TRANSMEM 268 290 POTENTIAL.
SQ SEQUENCE 880 AA; 102210 MW; 8AD99AB7B4E50671 CRC64;

Query Match 6.6%; Score 102; DB 1; Length 880;
Best Local Similarity 19.3%; Pred. No. 0.58;
Matches 58; Conservative 47; Mismatches 83; Indels 112; Gaps 13;

QY 47 LFKYWHYSITSLVYLIVKIQFMENRKPFTLKYPILWNGALAAFSIATIRFSID 106
Db 53 VFLTYLKHSLGFFPLEFIIFV-----PLFTNVAVRK-----VILEFHGE 93
QY 107 PLR-----SLYAGFYKTYLCYCNPTDV-----AATWSFAFALSKIV 143
Db 94 PLKIHPLADFGIAPTAALTAVKXWSSMLFYFNSSNFGVSDPIFGIDRAFYTFQLPLKIV 153

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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:21:03 ; Search time 60 Seconds
(without alignments)
1370.355 Million cell updates/sec

Title: US-09-936-845a-15
Perfect score: 1545
Sequence: 1 MELAFWMDLNTFTYGNH.....FFVKAYIKSKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545	100.0	291	3	AAB00198 Putative
2	564	36.5	435	3	AAB00199 Putative
3	547	35.4	269	3	AAB00205 Putative
4	492	31.8	270	4	AAB04173 Human gen
5	492	31.8	270	5	ABG32079 Human rec
6	492	31.8	270	5	AAB24550 Human ELG
7	492	31.8	270	5	ABB78813 Human NOV
8	492	31.8	270	5	ABB78812 Human NOV
9	492	31.8	270	5	ABP56418 Human LCE
10	492	31.8	270	5	ABB2960 Human LCE
11	492	31.8	270	6	ABB2966 Human LCE
12	485.5	31.4	278	3	AAY79263 Putative
13	485.5	31.4	278	5	AAY79269 Fruitfly
14	484.5	31.4	313	4	ABB60310 Drosophila
15	483.5	31.3	263	6	AAB37330 Human VLC
16	483	31.3	270	4	AAB04172 Human gen
17	479	31.0	271	3	AAY79260 Putative
18	479	31.0	271	4	ABA48959 Mouse fat
19	479	31.0	271	5	ABP56420 Human elc
20	479	31.0	272	3	AAY79249 Human put
21	478	30.9	271	3	AAB00209 Murine se
22	476.5	30.8	261	3	AAY79264 Putative
23	469	30.4	236	5	ABP56419 Human elc
24	469	30.4	236	6	ABB2959 Human LCE
25	451	29.2	269	5	ABB78814 GNS1/SUR4

26	437.5	28.3	265	5	AAE24555 Human ELG
27	435.5	28.2	265	3	AAY79266 Human elc
28	435.5	28.2	265	3	AB29648 Human mem
29	435.5	28.2	265	4	AU000476 Human INT
30	435.5	28.2	265	5	AAU87832 Human elc
31	435.5	28.2	265	5	AAU87832 Human elc
32	435.5	28.2	265	6	AAU87832 Human elc
33	435.5	28.2	265	6	ABO32607 Secreted
34	435.5	28.2	265	6	ABO32621 Human LCE
35	435.5	28.2	265	6	ABB2962 Human LCE
36	435.5	28.2	265	6	ABB2961 Human LCE
37	434.5	28.1	240	4	ABO07183 Human p53
38	433	28.0	216	4	AAU93344 Human pol
39	433	28.0	216	5	AAU93344 Human pol
40	424	27.4	216	4	ABG64366 Human alb
41	424	27.4	216	5	ABG64366 Human alb
42	413.5	26.8	219	6	ABO32609 Secreted
43	398	25.8	274	3	ABO00200 Putative
44	374	24.2	274	3	ABO00202 Putative
45	370.5	24.0	297	4	AB86466 Thraustoc

ALIGNMENTS

RESULT 1
AAB00198
ID AAB00198 standard; protein; 291 AA.
XX
AC AAB00198;
DT
DT 08-FEB-2001 (first entry)
XX
DE Putative polynunsaturate fatty acid elongase (PUFA).
XX
KW Elongase; polynunsaturate fatty acid; PUFA; dietary supplement;
KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
KW docosahexaenoic acid; docosapentaenoic acid; docosahexaenoic acid.
XX
OS Caenorhabditis elegans.
XX
PN WO200005330-A1.
XX
PD 21-SEP-2000.
XX
PF 20-MAR-2000; 2000WO-GB001035.
XX
PR 18-MAR-1999; 99GB-00006307.
XX
PR 18-FEB-2000; 2000GB-00003869.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Napier JA;
XX
DR WPI; 2000-647074/62.
XX
PT Novel isolated polypeptide comprising functional long chain
PT polynunsaturate fatty acid (PUFA) elongase of Caenorhabditis elegans used
PT to produce PUFA for foodstuff, dietary supplement or pharmaceutical
PT composition.
XX
PS Disclosure; Page 25; 42pp; English.
XX
CC New elongase polypeptides which are functional long chain polynunsaturated
CC fatty acid (PUFA) elongase polypeptides are described. The elongase
CC catalyses an elongase reaction to produce PUFA (a 24 carbon fatty acid
CC with at least 4 double bonds) such as di-homo-gamma-linoleic acid
CC (20:3Delta5,11,14), arachidonic acid (20:4Delta5,8,11,14),
CC eicosapentaenoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid
CC (22:3Delta3,15,19), docosapentaenoic acid (22:5Delta7,10,13,16),
CC docosahexaenoic acid (22:6Delta7,10,13,16,19) or docosahexaenoic acid
CC (22:6Delta7,10,13,16,19). PUFA produced is useful in foodstuffs,

CC dietary supplements and in pharmaceutical compositions which can then be
 CC used to elavate PUFA levels of an animal or plant
 XX
 SQ Sequence 291 AA;

Query Match 100.0%; Score 1545; DB 3; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2.7e-161;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAEFNDLNTFIYGNHTDMTKYKSYHPPGEQVADPOYWTILFQKYWHSTISV 60
 DB 1 MELAEFNDLNTFIYGNHTDMTKYKSYHPPGEQVADPOYWTILFQKYWHSTISV 60
 QY 61 LYFLIKVIOKFMENRKPFTLKYPILLWNGALAAFSIIATLRFSDPLRLSYAEGFYKTL 120
 DB 61 LYFLIKVIOKFMENRKPFTLKYPILLWNGALAAFSIIATLRFSDPLRLSYAEGFYKTL 120
 QY 121 CYSNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIFLHYHHAVALIYVHSGAEH 180
 DB 121 CYSNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIFLHYHHAVALIYVHSGAEH 180
 QY 181 TAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVTVTVOFTOMLAGVGTMMVKV 240
 DB 181 TAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVTVTVOFTOMLAGVGTMMVKV 240
 QY 241 KTEYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVIIKSSKSKSVKNE 291
 DB 241 KTEYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVIIKSSKSKSVKNE 291

RESULT 2

AAB00199
 ID AAB00199 standard; protein; 435 AA.

XX AC AAB00199;

XX DT 08-FEB-2001 (first entry)

XX DE Putative polyunsaturate fatty acid elongase (PUFA).

XX KW Elongase; polyunsaturated fatty acid; PUFA; dietary supplement;
 XX KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
 XX KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
 XX KW docosatetraenoic acid; docosapentaenoic acid; docosahexaenoic acid.

XX OS Caenorhabditis elegans.

XX PN WO200055330-A1.

XX PD 21-SEP-2000.

XX PF 20-MAR-2000; 2000WO-GB001035.

XX PR 18-MAR-1999; 99GB-00006307.

XX PR 18-FEB-2000; 2000GB-00003869.

XX PA (UYBR-) UNIV BRISTOL.

XX PI Napier JA;

XX DR WPI; 2000-647074/62.

XX PT Novel isolated polypeptide comprising functional long chain
 PT polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used
 PT to produce PUFA for foodstuff, dietary supplement or pharmaceutical
 PT composition.

XX PS Disclosure; Page 25-26; 42pp; English.

XX CC New elongase polypeptides which are functional long chain polyunsaturated
 CC fatty acid (PUFA) elongase polypeptides are described. The elongase
 CC catalyses an elongase reaction to produce PUFA (a 24 carbon fatty acid
 CC with at least 4 double bonds) such as di-homo-gamma-linoleic acid

CC (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14),
 CC eicosapentaenoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid
 CC (22:3Delta3,15,19), docosatetraenoic acid (22:4Delta7,10,13,16),
 CC docosapentaenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid
 CC (22:6Delta7,10,13,16,19). PUFA produced is useful in foodstuffs,
 CC dietary supplements and in pharmaceutical compositions which can then be
 CC used to elavate PUFA levels of an animal or plant
 XX
 SQ Sequence 435 AA;

Query Match 36.5%; Score 564; DB 3; Length 435;
 Best Local Similarity 42.0%; Pred. No. 4.4e-53;
 Matches 128; Conservative 45; Mismatches 86; Indels 46; Gaps 7;

QY 22 DMTKY---KSYHPPGEQVADPOYWTILFQKYWHSTISVLYFILI---KVI----- 69
 DB 5 DYNPKYGLNYSIFLPPFTSPDAFRSTTMQNHWTQSITASVYVAVIFGKKVLIYKK 64
 QY 70 -----QKE---MENRKPFTLKYPILLWNGALAAFSIIATLR 102
 DB 65 SRVITFESSLOWAIKRNKNSLNSSQMFQIMBKYPFQIDTFLFWNSFLAIFSLGFLR 124
 QY 103 FSDIDPLRLSYAEG--PYKTLCYSCNPTDVAAPWSFAPALSKIVELGDTNFIILKRPLIP 160
 DB 125 MTEPFVWSKSAEGNSFKYSICHSSVAQGVTFWTEQFAMSKLPELIDTIFIILKRPLIP 184
 QY 161 LHYTHPAVALIYVHSGAEHTAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVT 220
 DB 185 LHWYHVTVMYTHAYKDHSTAGRFIMWYGVHMYSYVALRSKFLPKQMANVVT 244
 QY 221 TVOTOMLAGVGTMMVKVKT--EYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVI 278
 DB 245 TLQLAQWVGVIIGTVIYIKSGEY---CQQTWDNLGICFGVYFTYFLLFANFFYHAYV 301
 QY 279 IKSSK 283
 DB 302 KKNR 306

RESULT 3

AAB00205
 ID AAB00205 standard; protein; 269 AA.

XX AC AAB00205;

XX DT 08-FEB-2001 (first entry)

XX DE Putative polyunsaturate fatty acid elongase (PUFA).

XX KW Elongase; polyunsaturated fatty acid; PUFA; dietary supplement;
 XX KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
 XX KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
 XX KW docosatetraenoic acid; docosapentaenoic acid; docosahexaenoic acid.

XX OS Caenorhabditis elegans.

XX FH Key Location/Qualifiers

XX FT Misc-difference 64

XX FT /note= "Any amino acid"

XX FT Misc-difference 95

XX FT /note= "Any amino acid"

XX FT Misc-difference 99

XX FT /note= "Any amino acid"

XX FT Misc-difference 192

XX FT /note= "Any amino acid"

XX PN WO200055330-A1.

XX XX 21-SEP-2000.

XX XX 20-MAR-2000; 2000WO-GB001035.

XX XX 18-MAR-1999; 99GB-00006307.

QY 227 MLAGVGITWVYKTEYKLPQOSVANLYAFVIVTFAILFIQFPVAYI---IKSSK 283
Db 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWFSILTYIWFILFAHPCQTYIRPKVAKT 267
QY 284 KSK 286
Db 268 KSQ 270

RESULT 5
ABG92079 standard; protein; 270 AA.
AC ABG92079;
XX 29-NOV-2002 (first entry)
DT Human receptors and membrane associated protein REMAP-22.
XX Human;
XX Human; receptor and membrane-associated protein; REMAP; atherosclerosis;
XX cardiovascular disorder; hypertension; congestive heart failure; oedema;
XX aneurysm; angina pectoris; ischaemic heart disease; lung disease; nausea;
XX rheumatic heart disease; chronic obstructive pulmonary disease; anaemia;
XX emphysema; bronchitis; gastrointestinal disorder; peptic ulcer; asthma;
XX Crohn's disease; lipid metabolism disorder; Fabry's disease; dementia;
XX pancreatitis; diabetes mellitus; hyperlipidaemia; autoimmune disorder;
XX inflammatory disorder; neurological disorder; Creutzfeldt-Jakob disease;
XX cell proliferative disorder; protein replacement therapy; adenocarcinoma;
XX developmental disorder; metabolic disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; multiple sclerosis; Cushing's syndrome; anxiety;
XX schizophrenia; Addison's disease; endocrine disorder; gene therapy; gout;
XX amnesia; cancer; leukaemia; lymphoma; myeloma; sarcoma.
XX Homo sapiens.
OS WO200263006-A2.
FN 15-AUG-2002.
PD 05-FEB-2002; 2002WO-US003968.
XX 06-FEB-2001; 2001US-0267201P.
XX 16-FEB-2001; 2001US-0269580P.
PR 09-APR-2001; 2001US-0282679P.
PR 02-MAY-2001; 2001US-0288239P.
PR 14-JAN-2002; 2002US-0348687P.
XX (INCY-) INCYTE GENOMICS INC.
XX Azimzai Y, Yue H, Ding L, Nguyen DB, Gandhi AR, Burford M;
PI Thangavelu K, Elliott VS, Ramkumar J, Yao MG, Lal PG, Tang TY;
PI Swarnakar A, Warren BA, Walla NK, Policky JL, Xu Y, Honchell CD;
PI Au-Young J, Baughn MK, Duggan BK, Lu DAM, Gietzen KJ, Hillmann JU;
PI Raumann BE, Lu Y, Sapperstein SK, Tran UK, Richardson TW;
PI Emerling BW, Hafalia AUA, Burrill JD, Marcus GA, Zingler KA;
PI Kable AE, Gorward AE;
XX WPI: 2002-627559/67.
XX N-PSDB; AS67800.
XX New human receptor and membrane-associated proteins and polynucleotides,
PT useful for diagnosing, treating or preventing cardiovascular disorders
PT (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
PT cancers.
XX Claim 2; Page 190-191; 262pp; English.
XX The present invention relates to a new receptor and membrane-associated
CC protein (REMAP). The polypeptide, polynucleotide and agonist are useful
CC for treating a condition associated with decreased expression of
CC functional REMAP. The antagonist is useful for treating a disease
CC associated with overexpression of functional REMAP. The anti-REMAP

CC antibody is useful for diagnosing a condition or disease associated with
CC the expression of REMAP. These polypeptides, polynucleotides, agonists
CC and antagonists are particularly useful for diagnosing, treating or
CC preventing cardiovascular (e.g. atherosclerosis, hypertension, aneurysms,
CC congestive heart failure, angina pectoris, or ischaemic or rheumatic
CC heart disease), lung (e.g. oedema, chronic obstructive pulmonary disease,
CC emphysema or bronchitis) gastrointestinal (e.g. nausea, peptic ulcer or
CC Crohn's disease), lipid metabolism (e.g. Fabry's disease, diabetes
CC mellitus or hyperlipidaemia), autoimmune/inflammatory (e.g. anaemia,
CC asthma, gout, pancreatitis or Crohn's disease), neurological (e.g.
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, Parkinson's disease, anxiety, schizophrenia or
CC amnesia), metabolic (e.g. Addison's disease), developmental (e.g.
CC Cushing's syndrome), endocrine or cell proliferative disorders (e.g.
CC cancers including adenocarcinoma, leukaemia, lymphoma, myeloma or
CC sarcoma). The present amino acid sequence represents a human REMAP
CC protein of the invention
XX

SQ Sequence 270 AA;

Query Match 31.8%; Score 492; DB S; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FQKIYVHSITISVLYPIIKVIQKFMENRKPFTLKYPLILMNGALAAFSIIATLRFSDP 107
Db 30 FEEVWATSPPIALYLVLAIVGQVYKRGKGFNLQGPLILWSFCLAIPIFSGAVRWGIM 89
QY 108 IRLSYAEGFYKILCY-SCNPTDVAATWSPALSKIVELGDTMFIILKRPILFLHYHH 166
Db 90 GTVLLTGLKQKTCFNFINDNSTVKFMSWVFLSKVIELGDTAFIILKRPILFIHWYH 149
QY 167 AAVLIYTVHSGAHTAGRFYILMNYFAHSLMYYTTSVAMGYRLPKVSMVTYVQTQ 226
Db 150 STVLVTSFGYKKNVPGAGFWYTNFVGHMYYTTLKAAVKKPKQLPMLTSLILQ 209
QY 227 MLAGVGITWVYKTEYKLPQOSVANLYAFVIVTFAILFIQFPVAYI---IKSSK 283
Db 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWFSILTYIWFILFAHPCQTYIRPKVAKT 267
QY 284 KSK 286
Db 268 KSQ 270

RESULT 6

AAE24550
ID AAE24550 standard; protein; 270 AA.

AC AAE24550;

XX 04-NOV-2002 (first entry)

DT Human ELG6 protein.

XX Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
KW PUPA disorder; cardiovascular disorder; articular cartilage degradation;
KW peripheral vascular disease; atherosclerosis; coronary artery disease;
KW inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
KW osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
KW acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
KW acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
KW postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
KW Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
KW autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
KW dyslipidaemia; atopic disorder; diabetes; ELG6.

OS Homo sapiens.

XX WO200244320-A2.

XX 06-JUN-2002.

PD

XX

QY 48 FQKVTHTSITISVLYFILLIKVQKEMENKFFTLKYLWNGALAAFSIATLRFSDP 107
DB 30 FEYWTATSPFIALIYLVLLAVGQNYKBERGFLNQLGPIILWSFCLALFSLGAVRWGIM 89
QY 108 LRSIYAEFGFKTLCY-SCNPTDVAAFWSFALSKIVELGDTWTFILIRKPLIFLHYHH 166
DB 90 GTVLLTGLKQTVCFINFDNNTSVKFSWVLLSKVIELGDTAFILIRKPLIFLHYHH 149
QY 167 AAVLIYTHSGAEHTAAGRFYILMNYFAHSLMVTYTVSANGVRLPKWVSMVTYVTTQ 226
DB 150 STVLVYTSFGYKXKVPAGGFVTFNFGVHAIMYTYTLKAAVKKPKMLPMLTISQILD 209
QY 227 MLAGVGITWVYKVKTEYKLPQQOSVANLYLAFVYVTFAILFIQPFVKAYI---IKSSK 283
DB 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWSPILMNTYFILLFAHFFCQYIIPKVKAKT 267
QY 284 KSK 286
DB 268 XSQ 270

RESULT 8
ABB78812
ID ABB78812 standard; protein; 270 AA.
AC ABB78812;
XX
XX
DT 29-JUL-2002 (first entry)
XX Human NOV6a protein sequence SEQ ID NO:18.
XX Human; NOV6a; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
XX anti-diabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
XX cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
XX metabolic pathway modulation; neoplastic; neurological disorder; asthma;
XX adenocarcinoma; prostate cancer; uterus cancer; immune response;
XX Crohn's disease; multiple sclerosis; Graft versus host disease;
XX chromosome 10.
XX
XX Homo sapiens.
XX
XX WO200230974-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-0301922.
XX
XX 12-OCT-2000; 2000US-0240113P.
XX 16-OCT-2000; 2000US-0240625P.
XX 16-OCT-2000; 2000US-0240637P.
XX 16-OCT-2000; 2000US-0240648P.
XX 16-OCT-2000; 2000US-0240662P.
XX 16-OCT-2000; 2000US-0240669P.
XX 16-OCT-2000; 2000US-0240703P.
XX 16-OCT-2000; 2000US-0240732P.
XX 16-OCT-2000; 2000US-0241190P.
XX 18-JAN-2001; 2001US-0262455P.
XX
XX (CURA-) CURAGEN CORP.
XX (MILL/) MILLET I.
XX
XX Grosse WM, Alsbrook JP, Lepley DM, Burgess CE, Mishra V;
XX Kekuda R, Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
XX Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
XX WPI; 2002-444172/47.
XX N-PSDB; ABN86918.
XX
XX New NOVX polypeptides and polynucleotides, useful for treating or
XX preventing a NOVX-associated disorder or a pathological state in a
XX subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
XX cancer or diabetes.

PS
XX
CC The present invention describes novel human proteins designated NOVX
CC (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV6sv are
CC cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC antiarteriosclerotic, cardiovascular, anti-diabetic, immunosuppressive and
CC neuroprotective activities, and can be used in gene therapy. The NOVX
CC sequences can be used in therapeutics, particularly for treating,
CC preventing or alleviating a NOVX-associated disorder or a pathological
CC state in a subject, particularly a human. These disorders include
CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation or diabetes. The NOVX
CC sequences are also useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC especially useful in therapeutic or prophylactic applications for
CC neoplastic or neurological disorders, and in the treatment of
CC adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC versus host disease. The present sequence represents the human NOV6a
CC protein from the present invention. NOV6a is located to chromosome 10
XX
SQ Sequence 270 AA;
Query Match 31.8%; Score 492; DB 5; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FQKVTHTSITISVLYFILLIKVQKEMENKFFTLKYLWNGALAAFSIATLRFSDP 107
DB 30 FEYWTATSPFIALIYLVLLAVGQNYKBERGFLNQLGPIILWSFCLALFSLGAVRWGIM 89
QY 108 LRSIYAEFGFKTLCY-SCNPTDVAAFWSFALSKIVELGDTWTFILIRKPLIFLHYHH 166
DB 90 GTVLLTGLKQTVCFINFDNNTSVKFSWVLLSKVIELGDTAFILIRKPLIFLHYHH 149
QY 167 AAVLIYTHSGAEHTAAGRFYILMNYFAHSLMVTYTVSANGVRLPKWVSMVTYVTTQ 226
DB 150 STVLVYTSFGYKXKVPAGGFVTFNFGVHAIMYTYTLKAAVKKPKMLPMLTISQILD 209
QY 227 MLAGVGITWVYKVKTEYKLPQQOSVANLYLAFVYVTFAILFIQPFVKAYI---IKSSK 283
DB 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWSPILMNTYFILLFAHFFCQYIIPKVKAKT 267
QY 284 KSK 286
DB 268 XSQ 270

RESULT 9
ABP56418
ID ABP56418 standard; protein; 270 AA.
AC ABP56418;
XX
XX 12-MAR-2003 (first entry)
XX Human elongase HSEL01-like protein SEQ ID NO:2.
XX Human; elongase; elongase HSEL01-like protein; enzyme; cytostatic;
XX anti-diabetic; antisthmatic; anti-HIV; antiparkinsonian; neurotropic;
XX neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
XX cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
XX metabolic disease; central nervous system disorder; COPD; dementia;
XX Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
XX Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
XX psychosis; attention deficit disorder; headache pain; migraine.

```
OS Homo sapiens.
XX WO200262974-A2.
XX 15-AUG-2002.
XX 07-FEB-2002; 2002WO-BP001262.
XX 08-FEB-2001; 2001US-0267135P.
XX (FARB ) BAYER AG.
XX Zhu 2;
XX WPI; 2002-636596/68.
XX N-PSDB; AB222162, AB222164, AB222165.
XX New isolated human elongase HSELO1-like polynucleotide and encoded
PT peptide, useful for treating, preventing and ameliorating diseases such
PT as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX Claim 25; Fig 2; 128pp; English.
XX The present sequence represents a human elongase HSELO1-like protein (I).
XX (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, neurotropic,
XX antiparkinsonian, neuroprotective, tranquilizer, antiemetic, and can be used
XX analgesic, neuroleptic and cerebroprotective activities, and can be used
XX in gene therapy. (I) can be used in the treatment of a disease, such as
XX cancer, diabetes, central nervous system (CNS) disorder, asthma,
XX metabolic disease or COPD. The human elongase HSELO1-like protein is
XX useful in preventing, treating or ameliorating the diseases cited above,
XX including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
XX Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
XX schizophrenia, psychosis, attention deficit disorders, pain associated
XX with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
XX also be useful in identifying test compounds that may act as activators
XX or inhibitors at the enzyme's active site, or in raising specific
XX antibodies that can block and effectively reduce its activity
XX
XX Sequence 270 AA;
Query Match 31.8%; Score 492; DB 5; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FOKYWHYSITISVLYPILIKVQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSDIP 107
Db 30 FEYWATSPFIALIYLVLIAGVQNYMKERKGNLQGPLILWSFCLAFSLGAVRWGMIM 89
QY 108 LRSLYABGFYKILCY-SCNPTDVAAPFWSFAPALS KIVELGDTMFIILRKPLIFLHYHH 166
Db 90 GTVLLTGLKQTCVCFINFDNSTVKFWSWFLSKVIELGDTAFIILRKPLIFLHYHH 149
QY 167 ANVLIYTHSGAEHTAAGRFYILMYFAHSLMYTYTVSANGYRLPKWVSMVTVTQTQ 226
Db 150 STVLVYTSFGYKVKPAGGFWVTMFGVHAIWYTYTLKAAVKKPKMLPMLITSQILQ 209
QY 227 MLAGVGITWVYKVKTEYKLPCCOOSVANLYLAFVIYVTFAILRQFFVKAYI---IKSSK 283
Db 210 MFVGAIVSILTYIWRDQ--GCHTTMEHLFWSPILMYTYFILFAHFFCQYIIRPKVAKT 267
QY 284 KSK 286
Db 268 KSK 270
RESULT 10
ABB82960
ID ABB82960 standard; protein; 270 AA.
XX AC ABB82960;
XX DT 14-APR-2003 (first entry)
```

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XX Human LCE related protein (sequence ID No. 10).
XX LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
KW cancer; human; enzyme.
XX Homo sapiens.
XX WO200299068-A2.
XX 12-DEC-2002.
XX 03-JUN-2002; 2002WO-US017739.
XX 05-JUN-2001; 2001US-0296076P.
XX 10-OCT-2001; 2001US-0328605P.
XX 15-FEB-2002; 2002US-0357253P.
XX 01-MAR-2002; 2002US-0361196P.
XX (EXEL-) EXELIXIS INC.
XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Karim FD, Keyes LN, Koblizek TI;
XX WPI; 2003-167338/16.
XX Identifying a candidate p53 pathway modulating agent for
XX diagnosing/treating cancer comprises detecting a test agent-biased
PT activity of an assay system comprising a purified long chain fatty acyl
PT elongase (LCE) polypeptide or nucleic acid.
XX Claim 13; Page 60-61; 69pp; English.
XX The invention relates to identifying a candidate p53 pathway modulating
XX agent that involves assaying a purified LCE (long chain fatty acyl
XX elongase) polypeptide or nucleic acid or its functionally active fragment
XX or derivative, with a test agent. The methods are useful for identifying
XX a candidate p53 pathway modulating agent, modulating a p53 pathway of a
XX cell, or a mammalian cell, diagnosing a disease in a patient, identifying
XX a candidate branching morphogenesis modulating agent, and modulating
XX branching morphogenesis in a mammalian cell. The diseases that can be
XX diagnosed are breast, colon, lung or ovary cancer having greater than 25%
XX expression level. The method is useful for manufacturing a medicament for
XX diagnosing or treating breast, colon, lung or ovary cancer. Sequences
XX ABB82959-966 represent human LCE related polypeptide sequences
XX
XX Sequence 270 AA;
Query Match 31.8%; Score 492; DB 6; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FOKYWHYSITISVLYPILIKVQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSDIP 107
Db 30 FEYWATSPFIALIYLVLIAGVQNYMKERKGNLQGPLILWSFCLAFSLGAVRWGMIM 89
QY 108 LRSLYABGFYKILCY-SCNPTDVAAPFWSFAPALS KIVELGDTMFIILRKPLIFLHYHH 166
Db 90 GTVLLTGLKQTCVCFINFDNSTVKFWSWFLSKVIELGDTAFIILRKPLIFLHYHH 149
QY 167 ANVLIYTHSGAEHTAAGRFYILMYFAHSLMYTYTVSANGYRLPKWVSMVTVTQTQ 226
Db 150 STVLVYTSFGYKVKPAGGFWVTMFGVHAIWYTYTLKAAVKKPKMLPMLITSQILQ 209
QY 227 MLAGVGITWVYKVKTEYKLPCCOOSVANLYLAFVIYVTFAILRQFFVKAYI---IKSSK 283
Db 210 MFVGAIVSILTYIWRDQ--GCHTTMEHLFWSPILMYTYFILFAHFFCQYIIRPKVAKT 267
QY 284 KSK 286
Db 268 KSK 270
```

```
RESULT 11
ABB82966
ID ABB82966 standard; protein; 270 AA.
XX
AC ABB82966;
XX
DT 14-APR-2003 (first entry)
XX
DE Human LCE related protein (GenBank Identifier No. GI17454617).
XX
KW LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
XX cancer; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO200299068-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017739.
XX
PR 05-JUN-2001; 2001US-0296076P.
XX
PR 10-OCT-2001; 2001US-0328605P.
XX
PR 15-FEB-2002; 2002US-0357253P.
XX
PR 01-MAR-2002; 2002US-0361136P.
XX
(PA EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plozman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Karim PD, Keyes LN, Koblicez TI;
XX
DR WPI; 2003-167338/16.
XX
PT Identifying a candidate p53 pathway modulating agent for
XX diagnosing/treating cancer comprises detecting a test agent-biased
XX activity of an assay system comprising a purified long chain fatty acyl
XX elongase (LCE) polypeptide or nucleic acid.
XX
PS Claim 13; Page 68-69; 69pp; English.
XX
This invention relates to identifying a candidate p53 pathway modulating
XX agent that involves assaying a purified LCE (long chain fatty acyl
XX elongase) polypeptide or nucleic acid or its functionally active fragment
XX or derivative, with a test agent. The methods are useful for identifying
XX a candidate p53 pathway modulating agent, modulating a p53 pathway of a
XX cell, or a mammalian cell, diagnosing a disease in a patient, identifying
XX a candidate branching morphogenesis modulating agent, and modulating
XX branching morphogenesis in a mammalian cell. The diseases that can be
XX diagnosed are breast, colon, lung or ovary cancer having greater than 25%
XX expression level. The method is useful for manufacturing a medicament for
XX diagnosing or treating breast, colon, lung or ovary cancer. Sequences
XX ABB82959-966 represent human LCE related polypeptide sequences
XX
SQ Sequence 270 AA;
Query Match 31.8%; Score 492; DB 6; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 POKWYISITSVYFLIKYQKPMENRKFYKYLWNGALAAFSIATIRPSIDP 107
DB 30 FEYWATSPFALTYLVLLVAVQYMKERGFNLQGLFWSFCLAFISILGAVRMWGM 89
QY 108 LRSVLAEGFYATLCV-SCNPTDVAAFWSFAFALS KIVELGDTMFIILRKPLIFHYHH 165
DB 90 GTVLLTGKLTQVCFINFDNSTVYKFSWVFLSKVIELGDTAIIILRKPLIFHYHH 149
QY 167 AAVLIYVTHSGAEHTAGRFILMNYFAHSLMYTYTYSANGYRLPKWMSMTVTUQTQ 226
DB 150 STVLVYTSFGYKKNVAGGFWVTWNFGVHAINTYTYTLKAAVXPPKMLFMTLSQILQ 209
QY 227 MLAGVGLTWYKVEYKLVKQSQSVANLYLAFVYVTEALIRTOFPVKAYI---IKSSK 283
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Db 210 MFVGAIVSILTYIWRDQ--GCHTTWEHLFWFSILYMTYFILFAHFFCQTYIRPKVKAKT 267
QY 284 KSK 286
Db 268 KSK 270

RESULT 12
AAV79263
ID AAV79263 standard; protein; 278 AA.
XX
AC AAV79263;
XX
DT 03-JUL-2000 (first entry)
XX
DE Putative Drosophila melanogaster homologue of elongase GLELO.
XX
KW elongase; GLELO; polyunsaturated fatty acid; eicosatetraenoic acid;
XX dihomogamma-linolenic acid; transgenic plant; transgenic animal.
XX
OS Drosophila melanogaster.
XX
PN WO200012720-A2.
XX
PD 09-MAR-2000.
XX
PF 30-AUG-1999; 99WO-US019715.
XX
PR 02-SEP-1998; 98US-00145828.
XX
(PA ABBO ) ABBOTT LAB.
XX
PI Mukerji P, Leonard AE, Huang Y, Thurmond J, Kirchner SJ;
PI Parker-Barnes JM, Das T;
XX
DR WPI; 2000-237881/20.
XX
Isolated nucleic acids encoding elongase enzymes for producing
XX polyunsaturated fatty acids that can be used to form nutritional
XX compositions.
XX
Example 15; Fig 41; 210pp; English.
XX
This sequence is that of a putative Drosophila melanogaster homologue,
XX termed DML, of Mortierella alpina polyunsaturated fatty acid (PUFA)
XX elongase GLELO (see AAV79243). It is the translation of a DNA fragment
XX identified in a database search using GLELO as query. The 2 sequences
XX show 27.2% identity in a 206 amino acid overlap. The invention provides
XX PUPA elongase nucleotide sequences and polypeptides that are involved in
XX the elongation of PUFAs, such as gamma-linolenic acid. The invention also
XX provides host cells, transgenic plants and transgenic animals expressing
XX an elongase, and methods for production of PUFAs, such as dihomogamma-
XX linolenic acid and eicosatetraenoic acid, for use in nutritional,
XX pharmaceutical, cosmetic and animal feed compositions
XX
SQ Sequence 278 AA;
Query Match 31.4%; Score 485.5; DB 3; Length 278;
Best Local Similarity 37.7%; Pred. No. 1.1e-44;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;
QY 23 MTKYKYSYHFGQVADP-----QYTILFKQYHSHSITISVLFIKVIQKPMENR 76
DB 11 VTPNYSYIDFENDFIHQTRKWLLENWTVF---YYCGI-----YMLVIFGQHFQMR 62
QY 77 KPTLKYPLWNGALAAFSIATIRP3DIPRLSVAEGFYKLYCYS--CNPTDVAAFWS 134
DB 63 PRQLAGPLIIWNTLLAMFSIMGAARTAPELIHVLFHYGLFHSVCVPSVIEQDRVCGFWT 122
```



```

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU101840-ABU16175) and the encoded proteins (ABB57733-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ      Sequence 313 AA;
          Query Match           31.4%; Score 484.5; DB 4; Length 313;
          Best Local Similarity 37.7%; Pred. No. 1.6e-44;
          Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY    23 MTTKKYKSYHPGEOVADP-----QWTILFKQYWTHSITISLVFLIKLYOKEMNR   76
DB    :|::||:::||::||::||::||::||::||::||::||::||::||::||:
       S VTPNYSYIFDPENDPIHORTKKWLEKNTWTF---YYCGI-----YNLVI FGQHFNQR   56

QY    77 KEFTLKYEYLINWGALAAFSIIATLRFSIDPLASLAEGFYKTLQCS--CNPTDVAAPWS   134
DB    :|::||::||::||::||::||::||::||::||::||::||::||:
       57 PRFQLRGRLLIWNILLAMFSIMGAAARTAPELIHLVRHYGLFHSCVPVSIEQDRVCGFWT   116

QY    135 PAFALSKIVELGDWTFPIILRKRPLFIHYTHHAVLITYVHSAGETHAAGR FYILNMVFA     194
DB    :|::||::||::||::||::||::||::||::||::||::||::||:
       117 WLDFVLSKLPGDTGFI VLREQPLFIHLWHYHHITLVLYSWFSYTEYTSARFIWMNVCV   176

QY    195 HSLMTYYYTVSAMGYRLPKWYSMTVVTTQTOMLAGVGI -TNMVKYKTEYKLPCQQSVA     253
DB    :|::||::||::||::||::||::||::||::||::||::||::||:
       177 HSVMYSYALKARENPFPFSMITLSILAQMIGCAINMWANGFLXKTHTGSCHISOR   236

QY    254 NYLLAFVIYVTTAILFIQFFVKA YIIKSSKKSK   286
DB    :|::||::||::||::||::||::||::||::||::||::||::||:
       237 NNLNSIAMYSYVLFARFFPYKAYLAPGGHKSR   269
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[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2004, 15:29:04 ; Search time 48 Seconds
(without alignments)
1707.965 Million cell updates/sec

Title: US-09-936-845A-15

Perfect score: 1545
Sequence: 1 MELAEFNDLNTFTTIGPNH.....FFVKAYIKSKKSKSVKNE 291

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545	100.0	291	15	US-10-369-493-5831
2	492	31.8	270	10	US-09-936-782-18
3	492	31.8	270	10	US-09-936-782-20
4	492	31.8	270	16	US-10-433-238-9
5	485.5	31.4	278	9	US-09-903-456-58
6	485.5	31.4	278	14	US-10-156-911-58
7	485.5	31.4	278	14	US-10-408-736-56
8	479	31.0	271	9	US-09-903-456-53
9	479	31.0	271	10	US-09-936-782-107
10	479	31.0	271	14	US-10-156-911-53
11	479	31.0	271	14	US-10-408-736-50
12	479	31.0	272	9	US-09-903-456-24
13	479	31.0	272	14	US-10-156-911-24
14	479	31.0	272	14	US-10-408-736-21
15	476.5	30.8	261	9	US-09-903-456-60

16	476.5	30.8	261	14	US-10-156-911-60	Sequence 60, Appl
17	476.5	30.8	261	14	US-10-408-736-58	Sequence 58, Appl
18	469	30.4	236	10	US-09-936-782-106	Sequence 106, Appl
19	451	29.2	269	10	US-09-976-782-37	Sequence 37, Appl
20	447.5	29.0	267	10	US-09-976-782-110	Sequence 110, Appl
21	435.5	28.2	265	9	US-09-903-456-64	Sequence 64, Appl
22	435.5	28.2	265	10	US-09-936-782-109	Sequence 109, Appl
23	435.5	28.2	265	10	US-09-936-782-109	Sequence 109, Appl
24	435.5	28.2	265	14	US-10-161-521A-4	Sequence 4, Appl
25	435.5	28.2	265	14	US-10-156-911-64	Sequence 64, Appl
26	435.5	28.2	265	14	US-10-408-736-62	Sequence 62, Appl
27	435.5	28.2	265	14	US-09-833-245-1115	Sequence 1115, Appl
28	433	28.0	216	11	US-09-833-245-1114	Sequence 1114, Appl
29	424	27.4	216	11	US-09-833-245-1114	Sequence 1114, Appl
30	413.5	26.8	219	10	US-09-936-782-108	Sequence 108, Appl
31	391	25.3	360	10	US-09-936-782-108	Sequence 108, Appl
32	360	23.3	265	9	US-09-903-456-55	Sequence 55, Appl
33	360	23.3	265	9	US-09-903-456-89	Sequence 89, Appl
34	360	23.3	265	14	US-10-156-911-55	Sequence 55, Appl
35	360	23.3	265	14	US-10-156-911-89	Sequence 89, Appl
36	360	23.3	265	14	US-10-408-736-52	Sequence 52, Appl
37	360	23.3	288	9	US-09-903-456-56	Sequence 56, Appl
38	360	23.3	288	9	US-09-903-456-62	Sequence 62, Appl
39	360	23.3	288	14	US-10-156-911-56	Sequence 56, Appl
40	360	23.3	288	14	US-10-156-911-62	Sequence 62, Appl
41	360	23.3	288	14	US-10-408-736-54	Sequence 54, Appl
42	360	23.3	288	14	US-10-408-736-60	Sequence 60, Appl
43	360	23.3	288	15	US-10-369-493-6094	Sequence 6094, Appl
44	356	23.0	174	10	US-09-936-782-243	Sequence 243, Appl
45	327.5	21.2	238	9	US-09-903-456-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-10-369-493-5831
; Sequence 5831, Application US/10369493
; Publication No. US0030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5831
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5831

Query Match 100.0%; Score 1545; DB 15; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.7e-152; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 0;

Qy 1 MELAEFNDLNTFTTIGPNHDMTKYKYSHPGQVADPQYWTILFQKYVHSTISV 60

Db 1 MELAEFNDLNTFTTIGPNHDMTKYKYSHPGQVADPQYWTILFQKYVHSTISV 60

Qy 61 LYLILKVIQKFMENRKPFTLKYPLILWNGALAFSIIATLRFISIDPLRLSYABGFYKTL 120

Db 61 LYLILKVIQKFMENRKPFTLKYPLILWNGALAFSIIATLRFISIDPLRLSYABGFYKTL 120

Qy 121 CYSCNPTDVAAPFWSAFALSKIVELGDMFTIILKRPILIFLHYVHAALVLYVHSGAEH 180

Db 121 CYSNPTDVAAFWSPAFALSKIVELGDTMFIILRKPLIFLHYHHAANVLIYTVHSGAEH 180

Qy 181 TAAGRFVILANYPFAHSLMYTYTVSANGYRLPKWVSMVTVTQTTQMLAGVGIITWVYKV 240

Db 181 TAAGRFVILANYPFAHSLMYTYTVSANGYRLPKWVSMVTVTQTTQMLAGVGIITWVYKV 240

Qy 241 KTEYKLPQCOOSVANLYAFVIYVTFALLFIQTFVKAYIILKSSKSKSVKNE 291

Db 241 KTEYKLPQCOOSVANLYAFVIYVTFALLFIQTFVKAYIILKSSKSKSVKNE 291

RESULT 2

US-09-976-782-18

; Sequence 18, Application US/09976782

; Publication No. US20030190715A1

; GENERAL INFORMATION:

; APPLICANT: Grosse et al

; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-157

; CURRENT APPLICATION NUMBER: US/09/976,782

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,113

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60/240,662

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,732

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,625

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,703

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/241,190

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,637

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,669

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/262,455

; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/240,648

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 18

; LENGTH: 270

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-976-782-18

Query Match 31.8%; Score 492; DB 10; Length 270;

Best Local Similarity 39.9%; Pred. No. 8.6e-43;

Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;

Qy 48 FQKYWHYSITISVLVYFIIKVIQKFMENKPFITLKYPLILWNGALAAFSIATLRFSDP 107

Db 30 FEEWATSPFIALIYLVLIANGQNYMKRGKFNLOGPILLWSFCLAFSILGAVRWGIM 89

Qy 108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSPAFALSKIVELGDTMFIILRKPLIFLHYHH 166

Db 90 GTVLLTGLKQTCVCFINFDNSFTVKFSWVLLSKVIELGDTAFIILRKPLIFLHYHH 149

Qy 167 AAVLIYTVHSGAEHTAAGRFVILANYPFAHSLMYTYTVSANGYRLPKWVSMVTVTQTTQ 226

Db 150 STVLVYTSFGYKXKVPAGCNFVTMFGVHAIMYTYTTLKAANYKPPKMLPMLITSQILQ 209

Qy 227 MLAGVGITWVYKVKTEYKLPQCOOSVANLYAFVIYVTFALLFIQTFVKAYI---IKSSK 283

Db 210 MFGVAIVSILTYINRQDQ--GCHTMEHLFWSFILMYTYFILFAHFFCQTYIRPKVKAKT 267

Qy 284 KSK 286

Db 268 KSQ 270

RESULT 4

US-10-433-238-9

; Sequence 9, Application US/10433238

; Publication No. US2004008699A1

; GENERAL INFORMATION:

; APPLICANT: Winther, Michael D

; APPLICANT: Knickle, Leah C

; APPLICANT: Haardt, Martin

; APPLICANT: Allen, Stephen J

RESULT 3

US-09-976-782-20

; Sequence 20, Application US/09976782

; Publication No. US20030190715A1

; GENERAL INFORMATION:

; APPLICANT: Grosse et al

; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-157

; CURRENT APPLICATION NUMBER: US/09/976,782

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,113

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60/240,662

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,732

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,625

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,703

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/241,190

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,637

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/240,669

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/262,455

; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/240,648

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 20

; LENGTH: 270

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-976-782-20

Query Match 31.8%; Score 492; DB 10; Length 270;

Best Local Similarity 39.9%; Pred. No. 8.6e-43;

Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;

Qy 48 FQKYWHYSITISVLVYFIIKVIQKFMENKPFITLKYPLILWNGALAAFSIATLRFSDP 107

Db 30 FEEWATSPFIALIYLVLIANGQNYMKRGKFNLOGPILLWSFCLAFSILGAVRWGIM 89

Qy 108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSPAFALSKIVELGDTMFIILRKPLIFLHYHH 166

Db 90 GTVLLTGLKQTCVCFINFDNSFTVKFSWVLLSKVIELGDTAFIILRKPLIFLHYHH 149

Qy 167 AAVLIYTVHSGAEHTAAGRFVILANYPFAHSLMYTYTVSANGYRLPKWVSMVTVTQTTQ 226

Db 150 STVLVYTSFGYKXKVPAGCNFVTMFGVHAIMYTYTTLKAANYKPPKMLPMLITSQILQ 209

Qy 227 MLAGVGITWVYKVKTEYKLPQCOOSVANLYAFVIYVTFALLFIQTFVKAYI---IKSSK 283

Db 210 MFGVAIVSILTYINRQDQ--GCHTMEHLFWSFILMYTYFILFAHFFCQTYIRPKVKAKT 267

Qy 284 KSK 286

Db 268 KSQ 270

```
; APPLICANT: Ponton, Andre
; APPLICANT: De Antueno, Roberto J
; APPLICANT: Jenkins, D K
; APPLICANT: Nwaka, Solomon O
; APPLICANT: Goldberg, Y Paul
; TITLE OF INVENTION: Human Elongase Genes, Uses Thereof, and Compounds for
; TITLE OF INVENTION: Modulating Same
; FILE REFERENCE: 330339-00004
; CURRENT APPLICATION NUMBER: US/10/433,238
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/253,728
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 270
; TYPE: PRT
; ORGANISM: human
US-10-433-238-9

Query Match      31.8%; Score 492; DB 16; Length 270;
Best Local Similarity 39.9%; Pred. No. 8.6e-43;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;

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DB 30 FEYWATSPPIALIVLIVLAVGQNTWKERKGNLQOPILILSFCIAISILCAVRMWGIM 89

QY 108 LRSVLAEGFYKTCY-SCNPTDVAAPFWSFAFALSXIVELGDTMPILRRKRLIFLHYHH 166
DB 90 GNVLLTGGLKQVCFINFDNFTVKFWSMVFLSKVIELGDTAFILRRKRLIFLHYHH 149

QY 167 AAVLYTVHSGAEHTAAGRFYILMVFASLHMYTVYSAMCYRLPKVSMVTVTQTO 226
DB 150 STVLVYTSFGYKXKVPAGGFWFMFGVHAINVYITLKAANNKPKMLDFMILSLQILQ 209

QY 227 MLAGVGITVMVYKATEYKLPQQSVANLYAFVYVTFAILFIQFFVKAYI---IKSK 283
DB 210 MFVGAIVSLITVWRQDQ--GCHTWEHLFWFSLVMTVYFILFAHFFCQYIRPKVAKT 267

QY 284 KSK 286
DB 268 KSG 270

RESULT 5
US-09-903-456-58
; Sequence 58, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235

US-10-156-911-58

Query Match      31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVILKVIQKFMENR 76
DB 11 VTPNYSYIFDFENDFIHQTRTKWLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

QY 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSRISYAEQFYKTCYS--CNPTDVAAPFWS 134
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; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58

Query Match      31.4%; Score 485.5; DB 9; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVILKVIQKFMENR 76
DB 11 VTPNYSYIFDFENDFIHQTRTKWLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

QY 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSRISYAEQFYKTCYS--CNPTDVAAPFWS 134
DB 63 PRFQRLGFLIWNLLANFSLMGARTAPSLIHVLRHYGLFHSVCVPSYISQDRVCGFWT 122

QY 135 FAFALSXIVELGDTMPILRRKRLIFLHYHAAVLYTVHSGAEHTAAGRFYILMVF 194
DB 123 WLFVLSKLPGLGDTFIVLRKQPLIFLHYHHITVLYSMFSTYETSSARWFIMVYCV 182

QY 195 HSLMYYTVYSAMCYRLPKVSMVTVTQTOMLAGVGI-TMVYKVKTEYKLPQQQSV 253
DB 183 HSNMYSYALKAAAFNPRFISMILTSIQLAQMIGCAINWANGFLKTHGTXSCHISOR 242

QY 254 NLYLAFVYVTFAILFIQFFVKAYIIRKSKSK 286
DB 243 NINLSIAMYSYFVLFARFFYKAYLAPGCHKSR 275

RESULT 6
US-10-156-911-58
; Sequence 58, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235

US-10-156-911-58

Query Match      31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVILKVIQKFMENR 76
DB 11 VTPNYSYIFDFENDFIHQTRTKWLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

QY 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSRISYAEQFYKTCYS--CNPTDVAAPFWS 134
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Db 63 PRFQRLGPLIWNLLAWFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
QY 135 PAFALSKIVELGDTWFIILKRPFLFLHYHAAVLIVTHSGAEHTAAGREYVILWNYFA 194
Db 123 WLFVLSKLELGDTPFIVLRKQPLFLHYHHTVLIYSWFSYTFETSSARWFIWNYCV 182
QY 195 HSLMVTYVTSAMGYLPRKWSNMTVTQTMLAGVGI-TWVYKVKTEYKLPCCQSV 253
Db 183 HSNVSYALKAAFPNPFISMIITSLQ-AQMIIIGCAINWANGFLKTHGTXSCHISOR 242
QY 254 NLYLAFVYVTFAILFIQFFVKAYIIKSKSK 286
Db 243 NINLSIAMYSYVFLFARFFYKAYLAPGGHKS 275

RESULT 7

US-10-408-736-56
; Sequence 56, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-408-736-56

Query Match 31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;
QY 23 MTKYKYSYHPPGGEQVADP-----QYMTILFQKYWYHSITISVLVFIKIKVQKWEHR 76
Db 11 VTPNYSYIFDFNDHFHQRTRKMKLENWTVF---YYCGI-----YMLVIFGQGHQNR 82
QY 77 KPFTLKYPILWNGALAAFSIATLRFSDPLSLVAEGFYKTLCS--CNPTDVAAPWS 134
Db 63 PRFQRLGPLIWNLLAWFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
QY 135 PAFALSKIVELGDTWFIILKRPFLFLHYHAAVLIVTHSGAEHTAAGREYVILWNYFA 194
Db 123 WLFVLSKLELGDTPFIVLRKQPLFLHYHHTVLIYSWFSYTFETSSARWFIWNYCV 182
QY 195 HSLMVTYVTSAMGYLPRKWSNMTVTQTMLAGVGI-TWVYKVKTEYKLPCCQSV 253
Db 183 HSNVSYALKAAFPNPFISMIITSLQ-AQMIIIGCAINWANGFLKTHGTXSCHISOR 242
QY 254 NLYLAFVYVTFAILFIQFFVKAYIIKSKSK 286
Db 243 NINLSIAMYSYVFLFARFFYKAYLAPGGHKS 275

RESULT 8

US-09-903-456-53
; Sequence 53, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-903-456-53

Query Match 31.0%; Score 479; DB 9; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41; 87; Indels 8; Gaps 4;
Matches 101; Conservative 47; Mismatches 47;
QY 49 QKVVYHSITISVLVFIKIKVQKWEHRKPTLKYPILWNGALAAFSIATLRFSDPL 108
Db 32 EYVWSSPLIVVYLLIVVGTVMTRKSPSLQRPILWSPFLAIFSILGTLRWKFWA 91
QY 109 RSLYAGFYKTLCSNPTD-VAAFWSPALSKIVELGDTWFIILKRPFLFLHYHHA 167
Db 92 TVMTVGLKQTCVPAIYTDADVRFWSFLFLSKVVELGDTAFILIRKPLIFVWYHHS 151
QY 168 AVLIVTVHSGAEHTAAGREYVILWNYFAHSLMVTYVTSAMGYLPRKWSNMTVTQTM 227
Db 152 TVLFTSFGYKVKVSPGGWMTMFGVHSVMYTYTMAAKLKHNPILPFWITSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQSVANLYLAFVYVTFAILFIQFFVKAYIIKSK-K 284
Db 212 VLGTIFGILNYIR---QEKGCHTTTEHFFNSFMYLYGYFILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 9

US-09-976-782-107
; Sequence 107, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2003-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190


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; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 107
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-782-107

Query Match      31.0%; Score 479; DB 10; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPLILWNGALAAFSIIATLRPSIDPL 108
Db 32 BEYVWSSFLIVVYLLIVVQGYMTRKSPSLQRPILWSPFLAIFSLGTLRMWKFWA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTWFIILRKRPILFLHYHHA 167
Db 92 TMTFTVGLKQIVCFPIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYYTYSAMGYRLPKWVSMVTVTQTOM 227
Db 152 TVLLFTSFGYKKNKVPSCGWFMTNFGVHVSVMYTYTAKAALKHPNLLPMWITSQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQOSVANLYLAFVIYVTFAILFTQFFVKAYIIKSSK-K 284
Db 212 VLGTIFGILNYIWR-----QKGCHTTTEHFFWSPMLYGTIFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 11
US-10-408-736-50
; Sequence 50, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-408-736-50

Query Match      31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPLILWNGALAAFSIIATLRPSIDPL 108
Db 32 BEYVWSSFLIVVYLLIVVQGYMTRKSPSLQRPILWSPFLAIFSLGTLRMWKFWA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTWFIILRKRPILFLHYHHA 167
Db 92 TMTFTVGLKQIVCFPIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYYTYSAMGYRLPKWVSMVTVTQTOM 227
Db 152 TVLLFTSFGYKKNKVPSCGWFMTNFGVHVSVMYTYTAKAALKHPNLLPMWITSQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQOSVANLYLAFVIYVTFAILFTQFFVKAYIIKSSK-K 284
Db 212 VLGTIFGILNYIWR-----QKGCHTTTEHFFWSPMLYGTIFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287

Query Match      31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPLILWNGALAAFSIIATLRPSIDPL 108
Db 32 BEYVWSSFLIVVYLLIVVQGYMTRKSPSLQRPILWSPFLAIFSLGTLRMWKFWA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTWFIILRKRPILFLHYHHA 167
Db 92 TMTFTVGLKQIVCFPIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYYTYSAMGYRLPKWVSMVTVTQTOM 227
Db 152 TVLLFTSFGYKKNKVPSCGWFMTNFGVHVSVMYTYTAKAALKHPNLLPMWITSQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQOSVANLYLAFVIYVTFAILFTQFFVKAYIIKSSK-K 284
Db 212 VLGTIFGILNYIWR-----QKGCHTTTEHFFWSPMLYGTIFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287

Query Match      31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPLILWNGALAAFSIIATLRPSIDPL 108
Db 32 BEYVWSSFLIVVYLLIVVQGYMTRKSPSLQRPILWSPFLAIFSLGTLRMWKFWA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTWFIILRKRPILFLHYHHA 167
Db 92 TMTFTVGLKQIVCFPIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYYTYSAMGYRLPKWVSMVTVTQTOM 227
Db 152 TVLLFTSFGYKKNKVPSCGWFMTNFGVHVSVMYTYTAKAALKHPNLLPMWITSQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQOSVANLYLAFVIYVTFAILFTQFFVKAYIIKSSK-K 284
Db 212 VLGTIFGILNYIWR-----QKGCHTTTEHFFWSPMLYGTIFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287
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Wed Jun 16 16:10:39 2004

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DB      268 SKS 270

RESULT 12
US-09-903-456-24
; Sequence 24, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1998-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24

Query Match      31.0%; Score 479; DB 9; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKWWHSITISLVLYFIILKVIQKFMENRKPFTLKYPILNNGALAAFSIATLRFSDPL 108
DB 32 EEWVSSFLIVVYLLLVGGQTYMTRKSFSLQRPILNLSFLLSILGTLRWKFWMA 91
QY 109 RSLYAGSFYKTLVCYCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPILFLHYHHA 167
DB 92 TMTFTVGLKQVCFALYTDVAVRFSFLSKVVELGDTAFILKRPILFVHWYHS 151
QY 168 AVLIYTVHSGAEHTAAGRFYILNMYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKVKVPGCGFWMTNFGVHSMVYTYTMTKAAKLKHPNLLPKVITSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPQQSVANLYLAFVIYVTFAILFIQFPVKAYTIKSSK-K 284
DB 212 VLGTIFGILNYWR-----QKGGCHTTTEHPFWSEFMYLGYTYFILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
DB 268 SKS 270

RESULT 14
US-10-408-736-21
; Sequence 21, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus

QY 49 QKWWHSITISLVLYFIILKVIQKFMENRKPFTLKYPILNNGALAAFSIATLRFSDPL 108
DB 32 EEWVSSFLIVVYLLLVGGQTYMTRKSFSLQRPILNLSFLLSILGTLRWKFWMA 91
QY 109 RSLYAGSFYKTLVCYCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPILFLHYHHA 167
DB 92 TMTFTVGLKQVCFALYTDVAVRFSFLSKVVELGDTAFILKRPILFVHWYHS 151
QY 168 AVLIYTVHSGAEHTAAGRFYILNMYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKVKVPGCGFWMTNFGVHSMVYTYTMTKAAKLKHPNLLPKVITSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPQQSVANLYLAFVIYVTFAILFIQFPVKAYTIKSSK-K 284
DB 212 VLGTIFGILNYWR-----QKGGCHTTTEHPFWSEFMYLGYTYFILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
DB 268 SKS 270

RESULT 13
US-10-156-911-24
; Sequence 24, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
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FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-10-408-736-21

Query Match 31.0%; Score 479; DB 14; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLVYFILLIKVQKFNKPTLKYPLILWNGALAAPSIIATLPSIDPL 108
DB 32 EYVWSSEFLIVVYLLLVGGTYMRTKRSQSLQRLWSPFLAIPESILGTLRWKFNMA 91

QY 109 RSLVAEGFYKILCYSCNPTD-VAAFWSPAFALSKEIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TWMTFTVLGLKQVCFALYITDDAVRFSFLFLSKVVELGDTAFILRLKRPILFLVHWHHS 151

QY 168 AVLIYTVHSGAHTFAAGRFYILMNFPAHSLMYTYTYSAMGYRLPKWVMTVTVTOTOM 227
DB 152 TVLLFTSEGYKNKVPSCGFMFMFNGVHSMVYTYTMMKAAKLGHPNLLPMTVITSLQILQM 211

QY 228 LAGV-GITWVYKTEKLPCCOSVANLYLAFVIYVTFAILPQFFVKAYIISKSSK-K 284
DB 212 VLGTFPGILNYIWR----QEKCHTTEHFWSPVLYGTYFILLFAHFFHRAVLYREKQVA 267

QY 285 SKS 287
DB 268 SKS 270

Search completed: June 16, 2004, 15:34:59
Job time : 49 secs

RESULT 15
US-09-903-456-60
; Sequence 60, Application US/09903456
; Patent No. US2002013874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Sun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1998-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (218)...(218)
; OTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60

Query Match 30.8%; Score 476.5; DB 9; Length 261;
Best Local Similarity 40.2%; Pred. No. 3.4e-41;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps 4;

QY 44 WTILFQKYWHSTISVLVYFILLIKVQKFNKPTLKYPLILWNGALAAPSIIATLRF 103
DB 21 WTWVP---YYCGI-----YMLVIFGGQHFQNRPRFQLRGPLIIMTWLLANFSIMGAAT 72

QY 104 SIDPLRSLVAEGFYKILCYSCNPTDVAFWSPAFALSKEIVELGDTMFIILRKRPILFL 161

73 APELIHVLHRHYGLFPHSVCVPSYIEQDRVCGFTWLFVLXKLPELGDTPIVLRKQPLIFL 132
162 HYTHHRAVLIYTVHSGAHTFAAGRFYILMNFPAHSLMYTYTYSAMGYRLPKWVMTVT 221
133 HWYHHITVLIYSWFSYTYETSSARWFIWMYCVHSMYSYALKAAEPNPRFISMIITS 192
222 VOTOMLAGVGI-TWVYKTEKLPCCOSVANLYLAFVIYVTFAILPQFFVKAYIISK 280
193 LQLAQMIIGCAINWANGPLKTHGTSCHISQRNINLSIAMYSYFVLFAFFFKAYLAP 252
281 SSKKSK 286
253 GCHKSR 258

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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:25:29 ; Search time 21 Seconds
(without alignments)
1332.940 Million cell updates/sec

Title: US-09-936-845A-15
Perfect score: 1545
Sequence: 1 MELAEFNDLNTFTTYGNH.....PFVKAYIIKSKKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB ID	Description
1	1545	100.0	291	2	S28299
2	564	36.5	435	2	T34200
3	398	25.8	274	2	T20786
4	374	24.2	274	2	H88690
5	360	23.3	288	2	T22789
6	329	21.3	281	2	T22791
7	327.5	21.2	286	2	B88690
8	281.5	18.2	328	2	T37734
9	262	17.0	345	2	S48517
10	235.5	15.2	334	2	T50139
11	230.5	14.3	310	2	S46638
12	220	14.2	347	2	S12916
13	191	12.4	158	2	T46257
14	128.5	8.3	868	2	T31527
15	117.5	7.6	1435	2	D96693
16	117	7.6	281	2	H96779
17	111.5	7.2	497	2	G86878
18	109.5	7.1	448	2	AH3095
19	109.5	7.1	448	2	B98191
20	105	6.8	729	2	A98320
21	105	6.8	729	2	A29263
22	105	6.8	861	2	T39714
23	103.5	6.7	330	2	T22293
24	102	6.6	880	2	D69427
25	99.5	6.4	510	2	G71365
26	99.5	6.4	919	2	S37786
27	98.5	6.4	443	2	A23634
28	97.5	6.3	498	1	JQ0026
29	97	6.3	219	2	P81365

30	96.5	6.2	272	2	T11689	NADH2 dehydrogenas
31	96	6.2	474	2	S41117	nitric-oxide reduc
32	95.5	6.2	407	2	D86782	peptidoglycan bios
33	95	6.1	782	2	E90427	hypothetical prote
34	95	6.1	2671	2	A49873	inositol 1,4,5-tri
35	94	6.1	271	2	T11692	NADH2 dehydrogenas
36	94	6.1	306	2	AC1174	conserved hypothet
37	93.5	6.1	759	2	A46188	cAMP-activated Na+
38	93	6.0	423	2	A90450	conserved hypothet
39	92.5	6.0	448	2	F95348	nitric-oxide reduc
40	92	6.0	291	2	T31962	hypothetical prote
41	92	6.0	308	2	AD1531	conserved hypothet
42	92	6.0	750	2	B83794	hypothetical prote
43	92	6.0	952	2	AG1209	B. subtilis yfho p
44	91.5	5.9	289	2	C69346	hypothetical prote
45	91.5	5.9	321	2	E90492	hypothetical prote

ALIGNMENTS

RESULT 1

S28299
hypothetical protein C40H1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Sep-1997
C:Accession: S28299
R:Berks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28299
A:Molecule type: DNA
A:Residues: 1-291 <BER>
A:Cross-references: EMBL:Z19154; NID:G6650; PID:G6654
C:Genetics:
A:Introns: 30/2; 68/1; 105/3; 177/1
C:Keywords: transmembrane protein

Query Match 100.0%; Score 1545; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MELAEFNDLNTFTTYGNHDTMTTKYKSYHFFGEQVADPOYTWILFKKYHSHITISV	60
DB	1	MELAEFNDLNTFTTYGNHDTMTTKYKSYHFFGEQVADPOYTWILFKKYHSHITISV	60
QY	61	LYFILIKVQKFMENKPTLKYPLILNKGALAAFSIATLRFSDPLRLSLVAEGFYKTL	120
DB	61	LYFILIKVQKFMENKPTLKYPLILNKGALAAFSIATLRFSDPLRLSLVAEGFYKTL	120
QY	121	CYSCNPTDVAAPFSAFALSKIVELGDTMFIILRKRLPLFLHYTHAAVLIYTVHSGAEH	180
DB	121	CYSCNPTDVAAPFSAFALSKIVELGDTMFIILRKRLPLFLHYTHAAVLIYTVHSGAEH	180
QY	181	TAAGRYILMNTFAISLMTYTVVSAMGYRLPKWYSMTVTVTQTMLAGVGLTWVYKV	240
DB	181	TAAGRYILMNTFAISLMTYTVVSAMGYRLPKWYSMTVTVTQTMLAGVGLTWVYKV	240
QY	241	KTEYKLPCCQSVANLYLAFVIYVTFALFIQFFVKAYIIKSKKSKSVKNE	291
DB	241	KTEYKLPCCQSVANLYLAFVIYVTFALFIQFFVKAYIIKSKKSKSVKNE	291

RESULT 2

T34200
hypothetical protein D2024.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R:Du, Z.; Gattug, S.
C:Accession: T34200
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid D2024.
A:Reference number: Z21488

QY 233 ITMWYKVKTEYKLP-COOSVANLYLAFVIYVTFAILFQFVKAYIIKSSKSKSVKNE 291
Db 216 IPGLHVFIKSADSVPCCAVSNVLSIGLMTYISLFLFAKFFKAYIQRS-PTKTSKOB 274

RESULT 4
H88690
protein F41H10.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
A:Accession: H88690
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/Projects/C_el
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a:
A:Accession: H88690
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAB03175.1; PID:gl397336; GSPDB:GN00022; CESP:F41H1
C:Genetics:
A:Gene: F41H10.8
A:Map position: 4

Query Match 24.2%; Score 374; DB 2; Length 274;
Best Local Similarity 30.4%; Pred. No. 1.6e-25;
Matches 83; Conservative 59; Mismatches 111; Indels 20; Gaps 6;

QY 22 DMTTKYKSYHFGBOVADPQYWTILFQKYVHSHITISVLVYFILIKVIOKFMENRKPFTL 81
Db 10 EVLITAPPSELSKXHIATQY-----AAFW-----ISMAYVVFGLKAVMTNRKPFDL 59

QY 82 KYPLILWNGALAAFSIIATLRFSDPLRSYABGEFKTLCYSCN-PTDVAATFWSAFALS 140
Db 60 TGPENLWAGLAIFSTGLSLATTFGLLHFFRGRGFESIHIIGDFYNGLSGHTWLFVLS 119

QY 141 KIVELGDTMFIILRKPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILANYPANSLMYT 200
Db 120 KYAEFGDTLFIILRKPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILANYPANSLMYT 179

QY 201 YTTVSAMGRVLPKWSMTVTQTTQMLAGVITTMWYKVKTEYKLPCCOOSVAN-----LY 256
Db 180 TYMLRSFGVKVPFWIAKNTITMOILQFV---ITHPIL-FHVGYLAVTQGVSDSTEGYTW 234

QY 257 LAFVIYVTFAILFQFVKAYIIKSSKSKSVK 289
Db 235 FCLLMREISVVLFGNPPYQSYIKGGGKFNAEK 267

RESULT 5
T22789
hypothetical protein F56H11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T22789
R:Wilkinson, J.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19616
A:Accession: T22789
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-288 <WIL>
A:Cross-references: EMBL:Z68749; PIDN:CAA92958.1; GSPDB:GN00022; CESP:F56H11.4
A:Experimental source: clone F56H11
C:Genetics:
A:Gene: CESP:F56H11.4
A:Map position: 4
A:Introns: 49/3; 110/1; 238/3
C:Superfamily: Saccharomyces probable membrane protein YCR034w

A:Accession: T34200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-435 <DUZ>
A:Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
C:Genetics:
A:Gene: CESP:D2024.3
A:Introns: 17/3; 57/3; 306/1; 398/3

Query Match 36.5%; Score 564; DB 2; Length 435;
Best Local Similarity 42.0%; Pred. No. 4.9e-42;
Matches 128; Conservative 45; Mismatches 86; Indels 46; Gaps 7;

QY 22 DMTTKY---KSYHFGBOVADPQYWTILFQKYVHSHITISVLVYFIL-----KVI----- 69
Db 5 DYNPKYGLENSIFLPETSDAFRSTWQNEHWQSITASVYVAVIFPGKGVLIYKK 64

QY 70 -----QKP--MENRKPFLKYPLILWNGALAAFSIIATL 102
Db 65 SRVITFESSIQNAIKRNRKSLNSSQMFQIMEKYKPFQDTPLPVWNSFLAIFSIILFLR 124

QY 103 FSDPLRSYABG--FYKTLCYSCNPTDVAATFWSAFALSKIIVELGDTMFIILRKPLIF 160
Db 125 NTFEFVWSNABGNSFKYSICHSSYAGVGTGFWTEQFANSKLPELIDTIFIVLRKPLIF 184

QY 161 LHYTHAAVLIYTVHSGAEHTAAGRFYILANYPANSLMYTYTVSANGYELPKWVSMYVT 220
Db 185 LHWYHVTVMYITWYHAYKHDTASGRWFIMWYGVHAWMSYALRSUKFLPKQMAWVT 244

QY 221 TVQTTQMLAGVIGITVMYKVKYKT--EYKLPCCOOSVANLYLAFVIYVTFAILFQFVKAYI 278
Db 245 TLQLAQWVGVIGITVYIRKSGEY---CQQTWNLGLCGYVTFYFLAFANFFYHAYV 301

QY 279 IKSKK 283
Db 302 KXNR 306

RESULT 3
T20786
hypothetical protein F1E6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20786
R:Matthews, L.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19324
A:Accession: T20786
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <WIL>
A:Cross-references: EMBL:Z81058; PIDN:CAB02921.1; GSPDB:GN00022; CESP:F1E6.5
C:Genetics:
A:Gene: CESP:F1E6.5
A:Map position: 4
A:Introns: 38/3; 99/1; 183/2; 235/2

Query Match 25.8%; Score 398; DB 2; Length 274;
Best Local Similarity 37.1%; Pred. No. 1.2e-27;
Matches 89; Conservative 48; Mismatches 99; Indels 4; Gaps 4;

QY 55 S-TISVLVYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSDPLRSYAE 114
Db 36 SYKIMIGLVITVYFGQKLMAHRKPDQLNTLALWFGFSLFSGIAAYKLIPELFGVPMKD 95

QY 115 GFYXTLCYSCN-PTDVA-AFWSAFALSKIIVELGDTMFIILRKPLIFLHYHAAVLIY 172
Db 96 GFVASVQENNYTDASTGFGWAFVMSKABELGDTMFLVLRKPLIFPMWYHALLTFVY 155

QY 173 TVHSGAEHTAAGRFYILANYPANSLMYTYTVSANGYELPKWVSMYVTQTTQMLAGV 232
Db 156 AWTYSEHQAWRWSLALNLAHTWYFPAVRALNIQTPEFVAKFITTIQIVQVISCY 215

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Query Match      23.3%; Score 360; DB 2; Length 288;
Best local Similarity 31.3%; Pred.No. 2.9e-24;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY      48  FQKYVHSITISVLVYFLIKVIOKFMENRKPFTLKYPILILWNGALAAFSIIATLRFSDIP 107
Db       40  FADHFDVTIQASILYVYVFGTKWFENRQPFQLTIFLNIWNFIILAAFSIAGAVKMTPEF 99

QY      108  LRSIYASGFTYKLYCSCNPT-DVNAFWSFAPALSKIIVELGDTWFIILIRKPLIFLHVYHH 166
Db       100  FGTIANKGIVASVCKVDFDFTKGNGYVWVLFMAASKLFDLVDTIFLVRKGPLMLPLHWYHH 159

QY      167  AAVLIIVTHSGAHTAAGRFVILMNYFAHSLMYTYTVVSAMGYRLPKWVSMTVTVTQTQ 226
Db       160  ILTWIYAWYSHPLTEGCFNRKGYILNVVVFHAFMSYFELRSKMKIRVPGPIAAQITSLQIVQ 219

QY      227  MLAGVGITVMYVYKTEYKPLCOOSVANLYLAFVIYVTFALLTFQFPVKYVIKSSK-KS 285
Db       220  FIFSCAVLAHLGYLMHFTNANCDPEPSVFKLAVFMDITYLALFVNFLLQSVYLRGGDKY 279

QY      286  KSV 288
Db       280  KAV 282

RESULT 6
T22791
hypothetical protein F56H11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22791
R:Wilkinson, J.
Submitted to the EMBL Data Library, January 1996
A:Reference number: Z19616
A:Accession: T22791
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-281 <WIL>
A:Cross-references: EMBL:Z68749; PIDN:CAA92360.1; GSPDB:GNO0022; CESP:F56H11.3
A:Experimental source: clone F56H11
C:Genetics:
A:Gene: CESP:F56H11.3
A:Map position: 4
A:Introns: 71/3; 132/1; 178/2; 215/2; 266/2

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Query Match      21.3%; Score 329; DB 2; Length 281;
Best Local Similarity 31.7%; Pred. No. 1.5e-21;
Matches 77; Conservative 49; Mismatches 93; Indels 24; Gaps 7;

QY      42 QYWTIL-----FKYMYHSITISVLYPILIKVIQKFMENRKPFTLKYP LI 86
Db      41 ELNSLLTNQDEVPEPHIRARFIQEHFGLFVQMAIYAVILVPSIKRFMRDREPFQLTALR 100

QY      87 LNWGALAAPSIIAT---LRSIDPLRSIYABGFYKTLICYS--CNFTDVAAFWSAFALSKI 142
Db      101 LWNFFLSVFIYGSWTWPPFVQOIR-LY--GLYCGCGEALNSLPDAQEYWLFIUTILSKA 157

QY      143 VELGDTWFIILRKPLIFLHYTHAAVLIIYTVHSGAEHAGRIYIILMNYFAHSLMITYY 202
Db      158 VEFVDTFFVLRLKKPLIFLHWYHEMATVFVFCNSNYPTSSQSRGVGVNLVFVHAFFMYPY 217

QY      203 TVSNAGVELERKWSMTVTYTTQTCMLAGV-GITWYVKKVKI-EYKLPQQQSVAANLYLAFV 260
Db      218 FTRSMNLKVPAKISMAVTVLQTLQFNCFIYCGTLMYISLATNQARYSNPFTQCLSYT 277

QY      261 IYV 263
Db      278 LHL 280

```

RESULT 7
E88690
protein F41H10.7 [imported] - Caenorhabditis elegans

C;Species: *Caenorhabditis elegans*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E38690
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A;Reference number: A75000; MUID:99049613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A;Accession: E38690
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <STO>
A;Cross-references: GB:chr_IV; PIDN:AB03174.1; PID:g1397335; GSPDB:GN000022; CESP:F41H1
C;Genetics:
A;Gene: F41H10.7
A;Map position: 4

Query Match	21.2%	Score	327.5	DB 2	Length	286			
Best Local Similarity	32.8%	Pred. No.	2.1e-21						
Matches	80	Conservative	44	Mismatches	109	Indels	11	Gaps	16
QY	55	SITISVLYFIILIKVIOKFMENRPFITKYPILIIWNGALAAFSIIATIRPSIDPLRS-LYA	113						
DB	38	SAKLAVCIATIFGLXVYWKDKAFDLSITELNIWNGILSTFSLGLFL-FTFPILLSVIRK	96						
QY	114	BGPYKILCY--SCNPIDVAAFNSFAFALSKIIVELGDTMPILIKRPLIFLFIYVHHAAVL	171						
DB	97	DGFSHTYSHVSELYSTDSGYWIFLWISKIPELDTVFIVLKRPLIFMGWHHAUTGY	156						
QY	172	YTV---HSGAEHTAAGRFIILMNYFPAHSLAVYTYTYSAMGYRLPKWVSMVTVTITQTOML	228						
DB	157	YALVCYHEDAVHMV---VVVMYNYIIHAPMYGYLLKSLKVPVPPSVAQAITTSQVQFA	213						
QY	229	AGV-GITWVYVYKVTYKLPCCQSVANLYLAFVIYVTFATLFIQFPFKVYIIKSSKSKS	287						
DB	214	VALPAQVHSYKHYHVEGVEGLAVSFRGTAIGFPMILTYFYFLWITQFYKHYLKGKGYNL	273						
QY	288	VQNE	291						
DB	274	AKDQ	277						

RESULT 8

T37734
SUR4 family protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T37734; T39101
R:Wedler, H.; Duesterhoft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21742
A:Accession: T37734
A:Status: preliminary; translated from GH/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-328 <MED>
A:Cross-references: EMBL:AL117213; PIDN:CAB55289.1; GSPDB:GN00066; SPDB:SPAC1639.01c
A:Experimental source: strain 972h-; cosmid c1639
R:Wedler, H.; Duesterhoft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21827
A:Accession: T39101
A:Status: preliminary; translated from GH/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-328 <WE2>
A:Cross-references: EMBL:AL117212; PIDN:CAB55288.1; GSPDB:GN00066; SPDB:SPAC806.09c
A:Experimental source: strain 972h-; cosmid c806
C:Genetics:
A:Gene: SPAC806.09c; SPAC1639.01c
A:Map position: 1
A:Introns: 5/2; 125/3
C:Superfamily: Saccharomyces probable membrane protein YCR034w

Query Match 18.2%; Score 281.5; DB 2; Length 328;
Best Local Similarity 31.0%; Pred. No. 2.7e-17;
Matches 76; Conservative 36; Mismatches 110; Indels 23; Gaps 6;

QY 57 TISVLPFILIKVIQKFMENRKPFTLKVPPLILWGLAALAPGSIITLRFSDPLRSLYARGF 116
DB 40 TIIISYVLLILVGRINRQPIRLOKIFQYVNLTSIASAILLALIFQVADAIYKHGF 99
QY 117 YKTLCSNCPTDVAAFWSFAPALSKIVELGDTWPIILRKRPDLIFLHYHH--AAVLIYTV 174
DB 100 FFSICNEKAWTQPLVFLYYCAYISKFLELTDTFVLVRKKPLQFLHCYHGHGATAVLVYTTQ 159
QY 175 HSGAEHTAAGRFYLLWNYPAHSLWYTYVTSANGYRLP--KWSVMTVTTVQTTOMLAGVG 232
DB 160 IVG--RTSISWLIIEINLLVHTVTTTTYILVAKIRVFNKKG----VTRPQIVQFFADLC 213
QY 233 ITWVMVKVTKTEYKLP-----CQOSVANLYLAFVIYVTFPAILFIQFFVKAYIIKSSXK 284
DB 214 FIVFVAVTEVAYRLKFKYKACWGHCSGHPLAFCGLATISSYLVLFIVFVHTY-----KK 268
QY 285 SKSVK 289
DB 269 NAALK 273

RESULT 9

S48517

SUR4 protein - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein L8039.2; protein YLR372w; regulatory protein APAL; SRE1 prote
C/Species: Saccharomyces cerevisiae
C/Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text change 21-Jul-2000
C/Accession: S48517; S48238; S51390; A54902; S59600; S43122; S49468
R;Revardel, E.
submitted to the EMBL Data Library, May 1994
A/Reference number: S48517
A/Accession: S48517
A/Molecule type: DNA
A/Residues: 1-345 <REV>
R/Cross-references: EMBL:L28723; NID:g453567; PID:g453568
R/Silve, S.; Lepiatols, P.; Josse, A.; Dupuy, P.H.; Bonin, O.; Kaghad, M.; Caput, D.; Fe
submitted to the EMBL Data Library, October 1994
A/Description: Sterol isomerase is a target for the immunosuppressant SR 31747 in saccha
A/Reference number: S48238
A/Accession: S48238
A/Molecule type: DNA
A/Residues: 1-345 <SIL>
A/Cross-references: EMBL:X82033; NID:g558641; PID:g558642
R/Du, Z.
submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae cosmid 8039.
A/Reference number: S51377
A/Accession: S51390
A/Molecule type: DNA
A/Residues: 1-345 <DUZ>
R/Cross-references: EMBL:U19103; NID:g609404; PID:g609406; MIPS:YLR372w
R/Garcia-Arnanz, M.; Maldonado, A.M.; Mazon, M.J.; Portillo, F.
J. Biol. Chem. 269, 18076-18082, 1994
A/Title: Transcriptional control of yeast plasma membrane H(+)-ATPase by glucose. Clonin
A/Reference number: A54902; MUID:94299524; PMID:8027068
A/Accession: A54902
A/Molecule type: DNA
A/Residues: 1-34, 'D', '36-207, 'R', '209-329, 'PY', '332-345 <GAR>
R/Cross-references: GB:X78326; NID:g467697; PIDN:CAA55129.1; PID:g467698
R/Revardel, E.; Bonneau, M.; Durrens, P.; Aigle, M.
Biochim. Biophys. Acta 1263, 261-265, 1995
A/Title: Characterization of a new gene family developing pleiotropic phenotypes upon mu
A/Reference number: S59600; MUID:96004900; PMID:7548216
A/Accession: S59600
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-345 <REW>
R/Cross-references: EMBL:L28723; NID:g453567; PID:g453568
C/Genetics:

QY 223 OTTOMLAGVITWYKTEYK-----LP-----COOSVANLYLAPVIVVTAIFLFIQFV 274
DB 224 QIIQFVLDILCYFTGYSHIAFRPPWLPVHVGDCSGSLFAFFCGCVLSSVLFIFIGFY 283
QY 275 KAYIIKSKKKK 286
DB 284 NTYIKRGAKNQ 295

RESULT 11

S46638
probable membrane protein YCR034w homolog YJL196c - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein 00343; protein YJL196c
C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
A/Accession: S46638; S56983
R/Purnelle, B.; Coster, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994

A/Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
ase gene ACO1 and two homologues to chromosome III genes.

A/Reference number: S46621; MUID:95274326; PMID:7754713

A/Accession: S46638

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-310 <PU>

A/Cross-references: EMBL:X77688; NID:gl183992; PIDN:CAA54764.1; PID:GS47599

R/Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, September 1995

A/Reference number: S56977

A/Accession: S56983

A/Molecule type: DNA

A/Residues: 1-310 <PU>

A/Cross-references: EMBL:249471; NID:gl008410; PID:gl008411; MIPS:YJL196c

C/Genetics:

A/Gene: SGD:ELO1

A/Cross-references: SGD:S0003732; MIPS:YJL196c

A/Map position: 101

C/Superfamily: Saccharomyces probable membrane protein YCR034w

C/Keywords: transmembrane protein

Query Match 14.3%; Score 220.5; DB 2; Length 310;

Best Local Similarity 27.0%; Pred. No. 5.9e-12;

Matches 66; Conservative .48; Mismatches 111; Indels 19; Gaps 7;

QY 61 LYFLIKVIOKFMENRKPFTLKYPILLWNGALAFSIIATIRPSIDPLRSIYAGFYKTL 120

DB 71 MYVVFGRSLVSKCKPLKRFISQVHNLMLTSSVFLMLIYVEQMLPIVYRHGLYFV 130

QY 121 CYS---CNPTDVAAPFSPAFALSIVELGDTWFIILKRKPLIFLHYHHAALVLYTVHSG 177

DB 131 CNVESWTQPMETLYLNY---MTKFPVFPADTVLVLKRLTFLHTYHGTALLCYNQL 187

QY 178 AEHTAAGRFYILMNYFAHSLMYTYTVSANGYRLPKWVSMVTVTQTQ-MLAGVGTWM 236

DB 188 VGYTAVTVVPVTLNLAHVLVLYFLSASGIRV--WKAWVTFLQIVQPMFLDIVVYV 245

QY 237 VYK--VKTEYKLPQOQ-----SVANLYLAFVIVVTAIFLFIQFVYKAVIIKS-SKKSK 286

DB 246 LYQKIVAAFKNACTPQCEDCLGSAITAAAGAILTSYLFIFISFYIEVYKGSASGKK 305

QY 287 SVKN 290

DB 306 INKN 309

RESULT 12

S12916

probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YCR521

C/Species: Saccharomyces cerevisiae

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000

A/Accession: S12916; S40919; S19446

R/Thierry, A.; Fairhead, C.; Dujon, B.

Yeast 6, 521-534, 1990

A/Title: The complete sequence of the 8.2 kb segment left of MAT on chromosome III reve

A/Reference number: S12916; MUID:91181345; PMID:1964349

A/Accession: S12916

A/Molecule type: DNA

A/Residues: 1-347 <TH>

A/Cross-references: EMBL:X56909; NID:g4489; PIDN:CAA40226.1; PID:g4490

R/Wicksteed, B.L.; Roberts, A.B.; Sagliocco, F.A.; Brown, A.J.P.

Yeast 7, 761-772, 1991

A/Title: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces

A/Reference number: S40917; MUID:92133166; PMID:1776366

A/Accession: S40919

A/Molecule type: DNA

A/Residues: 1-347 <WIC>

A/Cross-references: EMBL:S78624; NID:g244237; PIDN:AAB21360.1; PID:g244240

R/Dujon, B.; Fairhead, C.; Thierry, A.

submitted to the Protein Sequence Database, March 1992

A/Reference number: S19446

A/Accession: S19446

A/Molecule type: DNA

A/Residues: 1-347 <DUJ>

A/Cross-references: EMBL:X59720; NID:gl907116; PID:gl907176; MIPS:YCR034w

C/Genetics:

A/Gene: SGD:FEN1

A/Cross-references: SGD:S0000630; MIPS:YCR034w

A/Map position: 3R

C/Superfamily: Saccharomyces probable membrane protein YCR034w

C/Keywords: transmembrane protein

P/67-84/Domain: transmembrane #status predicted <TM1>

P/110-129/Domain: transmembrane #status predicted <TM2>

P/151-169/Domain: transmembrane #status predicted <TM3>

P/198-214/Domain: transmembrane #status predicted <TM4>

P/236-254/Domain: transmembrane #status predicted <TM5>

P/275-299/Domain: transmembrane #status predicted <TM6>

Query Match 14.2%; Score 220; DB 2; Length 347;

Best Local Similarity 28.2%; Pred. No. 7.4e-12;

Matches 67; Conservative 36; Mismatches 121; Indels 14; Gaps 5;

QY 62 YFLIKVIOKFMENRKPFTLKYPILLWNGALAFSIIATIRPSIDPLRSIYAGFYKTL 121

DB 78 YVYVIFGRFLSKSPFKLNGLFQLHNLVLTSLSLTLLMLVLEQLVPIIVQHGLYFAIC 137

QY 122 YSCNPTDVAAPFSPAFALSIVELGDTWFIILKRKPLIFLHYHH--AAVLYTVHSGAE 179

DB 138 NIGANTQPLVTLVYMYVIVKPIEIDTFVLVKKKLTFLHTYHGTALLCYTQMGF- 196

QY 180 HTAAGRFYILMNYFAHSLMYTYTVSANGYRLPKWVSMVTVTQTQMLAGVG-ITWVY 238

DB 197 -TSISWVPISNLGVHVMVWYVFLAARGIRV--WKKEWTRFQIIQFVLDIGFIYPAVY 253

QY 239 KVTEYKLP-----COOSVANLYLAFVIVVTAIFLFIQFVYKAVIIKSKSKSVK 289

DB 254 QKAVHLYFPLPHCGDCVCGSTTATFAGCATISSYLVLFISFINVYKRGKTKTSRVK 311

RESULT 13

T46257

hypothetical protein DKFZp7610031.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Nov-2000

C/Accession: T46257

R/Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A/Reference number: 223031

A/Accession: T46257

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-158 <AAA>

A/Cross-references: EMBL:AL137506

A/Experimental source: adult amygdala; clone DKFZp7610031

C/Genetics:

Search completed: June 16, 2004, 15:29:33
Job time : 23 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	659.5	42.7	286	5	Q9NAC6	Q9nac6	caenorhabdi
2	484.5	31.4	316	5	Q9VVB7	Q9vvb7	drosohila
3	447.5	29.0	267	11	Q92015	Q92015	mus muscul
4	447.5	28.9	268	13	Q90286	Q90286	brachydani
5	446.5	28.9	267	11	Q92036	Q92036	rattus norv
6	439.5	28.4	267	11	Q8CE45	Q8ce45	mus muscul
7	435.5	28.2	265	4	Q9H5J4	Q9h5j4	homo sapien
8	434.5	28.1	240	4	Q9NCD1	Q9ncd1	homo sapien
9	398	25.8	274	5	Q9XVQ9	Q9xvq9	caenorhabdi
10	396.5	25.7	323	5	Q86LT1	Q86lt1	cryptospori
11	374	24.2	274	5	Q20303	Q20303	caenorhabdi
12	368	23.6	301	5	Q9GNX9	Q9gnx9	leishmania
13	360	23.3	288	5	Q20901	Q20901	caenorhabdi
14	329	21.3	281	5	Q20904	Q20904	caenorhabdi
15	327.5	21.2	286	5	Q20300	Q20300	caenorhabdi
16	323.5	20.9	296	5	Q86JMS	Q86jms	dictyosteli

DD 7 ERFKVWTGNNETIIYSPFEYDSTLLIE-----SWWDDLTMTHTFCKNHHFKSV 53

"The genome sequence of *Drosophila melanogaster*.";
[2]
RN Science 287:2185-2195(2000).
RP
RA SEQUENCE FROM N.A.
RA Celinker S.B., Adams M.D., Krontmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J.J., An H., Baldwin D., Bauman J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Kustins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J.J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler P.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP
RA SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celinker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krontmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP
RA SEQUENCE FROM N.A.
RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP
RA SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP
RA SEQUENCE FROM N.A.
RA Rice A.H., Page C., Duffy J.B.;
RT "Sequence analysis and characterization of baldspot.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP
RA SEQUENCE FROM N.A.
RA Jung A.G., Schaefer M.A.;
RT "The *noa* gene encodes a member of a widely distributed family of
RL integral membrane proteins in *Drosophila*.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[8]
RP
RA SEQUENCE FROM N.A.
RA STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J.J., Pacleb J.J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AS003526; AAF49430.2; -
DR EMBL: AF265295; AAF75771.1; -
DR EMBL: AF279258; AAG02080.1; -
DR EMBL: AF279257; AAG02080.1; JOINED.
DR FLYbase; AY061121; AAL28669.1; -
DR FLYbase; Fgdn003650; Baldspot.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006119; P:electron transport; IEA.
DR InterPro: IPR002076; GNS1_SUR4.
DR Fram: FPO1151; ELO; 1.
DR PROSITE: PS01188; ELO; 1.
DR Transmembrane.
SQ SEQUENCE 316 AA; 36829 MW; B741960F28D2A3AD CRC64;

Query Match 31.4%; Score 484.5; DB 5; Length 316;
 Best Local Similarity 37.7%; Pred. No. 7.9e-35;
 Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTKYKYSYHHPGEOVADP-----QYTWLIPQKWHYSITISVLVYFILIKVIOKPMENR 76
 DB 8 VFNYSYIFDENDSIHORTKRMLENWTWF---YYCGI-----YMLVIFGGQHFQNR 59

QY 77 KPFTLKYPILWNGALAAAFSIATLRFSDIPLSIYAEQFYKTLCS--CNFTDVAAPWS 134
 DB 60 PRFQLRGFLIIWNTLLAMFSGAARTAPELHLVLRHYGLPHSVCPVSYISQDRVCGFWT 119

QY 135 FAFALSKIVELGDTWFIILRRPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILMYFA 194
 DB 120 WLFVLSKLPELGDTFIYLRKQPLIFLHYHHTITVLIYSWFSYETYSARAFWIMYCV 179

QY 195 HSLMYTYTVSANGYRLPKWYMTVTVTQTMLAGVGI-TWVYKVKTEYKLPQQQSV 253
 DB 180 HSNVYSYALKAAEPNPRFISMITSQLAQMIIGCAINWANGFLKTHGTSSCHISQR 239

QY 254 NLYLAFLVYVTFALFIQFFVKAYIIKSSKSK 286
 DB 240 NINLSIAMYSYFVLFARFFYKAVLAPGGHKS 272

RESULT 3

Q920L5 PRELIMINARY; PRT; 267 AA.

AC Q920L5; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 25, Last annotation update)
 DE Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
 GN ELOVL6 OR FAE OR ICE OR XASR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CS7B16; TISSUE=Liver;
 RA Matsuzaka T., Shimano H.;
 RT "murine complete cds for new fatty acyl elongase similar to cig30 (U97107).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21576178; PubMed=11567032;
 RA Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D.;
 RT "Identification of a Mammalian Long Chain Fatty Acyl Elongase Regulated by Sterol Regulatory Element-Binding Proteins.";
 RL J. Biol. Chem. 276:45359-45366 (2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP Nagarajan R., Le N.H., Mahoney H., Azaki T., Milbrandt J.D.;
 RA "Deciphering Peripheral Nerve Myelination Using Schwann Cell Expression Profiling";
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CZSCH II; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB072039; BAB68544.1; -
 DR EMBL; AF053453; AALJ4239.1; -
 DR EMBL; AF480860; AAMJ3450.1; -
 DR EMBL; BC051041; AAH51041.1; -
 DR MGD; MGI:2156528; Elovic.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0016747; P:transferase activity, transferring groups o...; IDA.
 DR GO; GO:0030497; P:fatty acid elongation; IDA.

DR InterPro; IPR002076; GNSL_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 SQ SEQUENCE 267 AA; 31610 MW; 4026C9C33FDD023 CRC64;

Query Match 29.0%; Score 447.5; DB 11; Length 267;
 Best Local Similarity 36.9%; Pred. No. 1.2e-31;
 Matches 97; Conservative 50; Mismatches 109; Indels 7; Gaps 3;

QY 26 KYKYSYHHPGEOVADPQYTWLIPQKWHYSITISVLVYFILIKVIOKPMENRKPFTLK 85
 DB 10 EYEFKQFNEAIO---W---MQENWKKSFLFSALYAAFIQGRHLMNKRKAPFLRKL 63

QY 86 ILWNGALAAAFSIATLRFSDIPLSIYAEQFYKTLCS--CNFTDVAAPWSAFALSKIVE 144
 DB 64 VLASLTAVAFSIFCALRTGAYMLYILMTKLGKQSCVQDFYNGPVSXFWAYAFVLSKAP 123

QY 145 LGDTMFIILKRPILFHLHYTHAAVLIYTVHSGAEHTAAGRFYILMYFAHSLMYTYTV 204
 DB 124 LGDTFIILKRPILFHLHYTHAAVLIYTVHSGAEHTAAGRFYILMYFAHSLMYTYTV 183

QY 205 SAMGYRLPKWYMTVTVTQTMLAGVGI-TWVYKVKTEYKLPQQQSVANLYLAFLVYV 264
 DB 184 RAAGFVSRKFAFITLSQITQMLGCVINYLWNQHDNDCCYSHFQIFWSSLWYLS 243

QY 265 FALFIQFFVKAYIIKSSKSKS 287
 DB 244 YLVLFCHFFFEYAYIGVKVKATKA 266

RESULT 4

Q802X6 PRELIMINARY; PRT; 268 AA.

AC Q802X6; (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Similar to fatty acid elongase 2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046901; AAH46901.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR002076; GNSL_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 SQ SEQUENCE 268 AA; 31386 MW; CDD41ACAL1639928 CRC64;

Query Match 28.9%; Score 447; DB 13; Length 268;
 Best Local Similarity 36.2%; Pred. No. 1.4e-31;
 Matches 101; Conservative 60; Mismatches 100; Indels 18; Gaps 8;

QY 19 NHTDM---TTKYKYSYHHPGEOVADPQYTWLIPQKWHYSITISVLVYFILIKVIOKPMEN 75
 DB 2 NMTDFQLPTEYEFERHF-DERLAIE--W---MQDNWKKSFLFCGAVTVLVFGQHFQMD 55

QY 76 RKPFTLKYPILWNGALAAAFSIATLRFSDIPLSIYAEQFYKTLCS--CNFTDVAAP 132
 DB 56 QRLLDLKRLMMWSLSLAIFSIIICAVRTGCFMLYILSTSGFKQSCVQDFYNGP--ISKF 113

QY 133 WSEFALSKIVELGDTWFIILRRPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILMYFA 192
 DB 114 WACAFVLSKAPLPGDTMFIILRRKQPLIFLHYHHTITVLIYSWFSYETYSARAFWIMY 173

QY 193 FAHSLMYTYTVSANGYRLPKWYMTVTVTQTMLAGVGI-TWVYKVKTEYKLPQQQSV 252
 DB 174 TVHALMYSYAAARAAGLRVFKPCAILITSQIAQAMDLAVSALVYRWMDG--DCFSYL 231


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KW Hypothetical protein.
SQ SEQUENCE 265 AA; 31376 MW; 01234E0BEF6CE341 CRC64;
  Query Match      28.2%; Score 435.5; DB 4; Length 265;
  Best Local Similarity 35.8%; Pred. No. 1.4e-30;
  Matches 95; Conservative 54; Mismatches 103; Indels 13; Gaps 5;

QY 26 KYKSVHPGQGVADPOYTWILFQKYYHSHITISLVLYFILIYKVIQFMENKPEFTLKYP 85
DB 10 EYEFKQFNEAIQ---W---MQENWKSKFLSALYAAFIQGRHLMNKRKAFELRKPL 63

QY 86 ILNMGALAAFSIIATLRFSDPLSLYAGFYKTLCL---YSCNPTDYAAAFWSAFAPALSKI 142
DB 64 VLSLTLAVSIFGALGTAGAWYILMTKGLKOSVCDQGYNGP--VSKFWAYAFVLSKA 121

QY 143 VELGDTMFIILRKLPLFLHYHAAVLYIVHSGAEHTAAGRFYILMNYFAHSLMYTYV 202
DB 122 PELGDTIPIILRKQKFLFLHWHHTVLLVYSWYSYKDMVAGGWFMTMNVGVHAWMSYV 181

QY 203 TVSAMGVLPKWSMTVTVTOTOMLAGVITWMVYKTEYKLPQOOSVANLYLAFVIY 262
DB 182 ALRAAGFRVSRKFAFITISQITQMLMGCVVNYLVFCWMQHDQ--CHSHFQNIWFWSLMY 239

QY 263 VTFAILPIQPFVKAYIIKSKSKS 287
DB 240 LSVLVLPCHFPPEAYIGKWKTKA 264

RESULT 8
Q8NCD1
ID Q8NCD1 PRELIMINARY; PRT; 240 AA.
AC Q8NCD1
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein FL390332.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NEO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074813; BAC11225.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 28271 MW; 38A101DCF141818E CRC64;
  Query Match      28.1%; Score 434.5; DB 4; Length 240;
  Best Local Similarity 38.0%; Pred. No. 1.6e-30;
  Matches 92; Conservative 50; Mismatches 93; Indels 7; Gaps 3;

QY 49 QKWWHSITISLVLYFILIYKVIQFMENKPEFTLKYPILNMGALAAFSIIATLRFSDPL 108
DB 2 Q8NWKSKFLSALYAAFIQGRHLMNKRKAFELRKPLVLSLTAVFSIFGALRTGAYMV 61

QY 109 RSLYAGGFKYTLCL---YSCNPTDYAAAFWSAFAPALSKIYELGDTMFIILRKLPLFLHYH 165
DB 62 YILMTKGLKQSVCDQGYNGP--VSKFWAYAFVLSKAPELGDTIPIILRKQKFLFLHWH 119

QY 166 HAAVLYIVHSGAEHTAAGRFYILMNYFAHSLMYTYVTVSAMGVLPKWSMTVTVTOT 225
DB 120 HITVLLYSYKDMVAGGWFMTMNVGVHAWMSYVYALRAAGFRVSRKFAFITISQIT 179
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QY 226 QMLAGVIGITWMVYKVKTEYKLPQOOSVANLYLAFVIYVTFAILPIQPFVKAYIIKSKSKS 285
DB 180 QMLMGCVVNYLVFCWMQHDQ--CHSHFQNIWFWSLMYLSYLVLFCFFPEAYIGKWKTKT 237

QY 286 KS 287
DB 238 KA 239

RESULT 9
Q9XVQ9
ID Q9XVQ9 PRELIMINARY; PRT; 274 AA.
AC Q9XVQ9
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fl186.5 protein.
GN Fl186.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81058; CAB02921.1; -.
DR PIR; T20786; T20786.
DR WormPep; Fl186.5; CE19785.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01151; ELO; 1.
SQ SEQUENCE 274 AA; 31361 MW; 2CBB7DAS5F418D714 CRC64;
  Query Match      25.8%; Score 398; DB 5; Length 274;
  Best Local Similarity 37.1%; Pred. No. 3e-27;
  Matches 89; Conservative 48; Mismatches 99; Indels 4; Gaps 4;

QY 55 SITTSVLVYFILIYKVIQFMENKPEFTLKYPILNMGALAAFSIIATLRFSDPLSLYAE 114
DB 36 SYKIMIGYLVITYFGQKLMARXKPFDLQNTLALNFGSFLSGIAAYKLIPELFGVPMKD 95

QY 115 GFYKTLCYSCN-P7DVA-AFWSAFAPALSKIYELGDTMFIILRKLPLFLHYHAAVLY 172
DB 96 GFVASYCONENYTTDASTGFGWAFVMSKAPELGDTMFLVLRKPFVPMWYHVALTFVY 155

QY 173 TVHSGAEHTAAGRFYILMNYFAHSLMYTYVTVSAMGVLPKWSMTVTVTOTOMLAGV 232
DB 156 AVTYSEHQAWARWSLALNLAHVHTVYFAVRALNIQTPEPAKFITTIQIVQFVISCY 215

QY 233 ITWMVYKVKTEYKLP-CQOOSVANLYLAFVIYVTFAILPIQPFVKAYIIKSKSKSVKNE 291
DB 216 IFGHVLIKSDSPGCAVSNVLSIGLMIISYLFPAKFFYKAYIQRS-PIKSKQE 274

RESULT 10
Q86LT1
ID Q86LT1 PRELIMINARY; PRT; 323 AA.
AC Q86LT1
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative fatty-acyl elongase.
GN FAELO1.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
```



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Db 28 FDDYFDVLVYSEVLVYLIVPLGPKANESREPRRLRYLIAWNLALSFSLGCTIGVIML 87
QY 108 LRSLYAGSYKTLCSNCPDVA-----AFWSPAFALSKIVELGDTMFIILRKPLIFL 161
Db 88 MHSLEERGNYETTCY----LDKSLYDGLTFLWFAFLSKIPMLDTFVLVTKKPIIFL 143
QY 162 HYYHHAVALIYVHSGAHTAGRFYILMNYFAHSLMYTYTYTSAMGYR-LPKWYMTVT 220
Db 144 EHYHLTLTVFCWYAGYTLIAGVAFASWNYAVHYVYFELCSLGMKRLRPIAPIT 203
QY 221 TVQTTQMLAGVGITWMYVKTEYKLPCCQSVANLYLAFVIYVTFAILFIQFFKAYIIR 280
Db 204 GAQLLQMVVGTIIVLYTFYGYISERGCGVDHRTIRMGLCMTGYSVFLFATLFLVRLY-MK 262
QY 281 SSKSKSVKNE 291
Db 263 KGAVTKSRKE 273

RESULT 13
Q20901 PRELIMINARY; PRT; 288 AA.
AC Q20901;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE LONG chain POLYUNSATURATED fatty acid elongation enzyme.
GN CEEL01 OR F56H11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Das T., Parker-Barnes J.M., Thurmond J.M., Bobik E., Leonard A.E.,
RA Chuang L., Huang Y.-S., Mukerji P.;
RT "Identification and characterization of novel polynunsaturated fatty
RT acid elongating enzymes from Mortierella alpina and Caenorhabditis
RT elegans."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244356; RAF70462.1; -.
DR EMBL; 268749; CAA92958.1; -.
DR PIR; T22789; T22789.
DR WormPep; F56H11.4; CE05979.
DR GO; GO:0015021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
SQ SEQUENCE 288 AA; 33561 MW; 8BA5CD4892012B0E CRC64;

Query Match 23.3%; Score 360; DB 5; Length 288;
Best Local Similarity 31.3%; Pred. No. 7.2e-24;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQYVHSTITISVLPIIKVIOKFMENRKPFTLYPLIMNGALAAFSIIATLRFSDIP 107
Db 40 FADHPDVTIQASILYMWVFGTKWFMNRQPFQLATPLINWFIILAAFSIAGAVMTPEF 99
QY 108 LRSLYAGSYKTLCSNCPNT-DVAAPWSPAFALSKIVELGDTMFIILRKPLIFLHYHH 166
Db 100 FGTIANKGIVASVCKVDFETKGENGYWVWFLFWASKLFEVLVDITFLVLRKRLMFLHWYHH 159
QY 167 AVALIYVHSGAHTAGRFYILMNYFAHSLMYTYTSAMGYR-LPKWYMTVTVVQTTQ 226
Db 160 ILTMIIYAWYSHPLTPGFENYGIYLVFVHAPMYVYFLFSMKIRVPGPIAQAITSLQIVQ 219
QY 227 MLAGVITWMYVKTEYKLPCCQSVANLYLAFVIYVTFAILFIQFFKAYIIRKSK-KS 285
Db 220 FIISCAVLHGLYMEFTNANCDPESVFKLAVFMDTTYLALFVNFPLQSVYLRGGDKY 279
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QY 286 KSV 288
Db 280 KAV 282

RESULT 14
Q20904 PRELIMINARY; PRT; 281 AA.
AC Q20904;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE F56H11.3 protein.
GN F56H11.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; 268749; CAA92960.1; -.
DR PIR; T22791; T22791.
DR WormPep; F56H11.3; CE16144.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
SQ SEQUENCE 281 AA; 33141 MW; 825DS29D7FEBF936 CRC64;

Query Match 21.3%; Score 329; DB 5; Length 281;
Best Local Similarity 31.7%; Pred. No. 3.9e-21;
Matches 77; Conservative 49; Mismatches 93; Indels 24; Gaps 7;

QY 42 QYWTIL-----FQYVHSTITISVLPIIKVIOKFMENRKPFTLYPLI 86
Db 41 ELWSLLTNQDEVPFHIRARRFIQHPGLFVQMAIYVILVFSIKRFMRDRFPQLTALR 100
QY 87 LNWGALAAFSIIAT---LRFSIDPLRSIYAGFYKTLCSY-CNPTDVAAPWSPAFALSKI 142
Db 101 LWNFPLSVFSIYGSWTMFPFMVQOIR-LY--GLYCCGCEALSNLPSQAEYVNLFLTILSKA 157
QY 143 VELGDTMFIILRKPLIFLHYHHAVALIYVHSGAHTAGRFYILMNYFAHSLMYTYTY 202
Db 158 VEFVDTFPLVLRKKFLIFLHWYTHMATVFPFCSNYTPTSSQSRGVIVNLVFWHAPMYPY 217
QY 203 TVSANGVELPKWVMYTVTCTTOMLAGV-GITWVYKVKVT-BYKLPCCQSVANLYLAFV 260
Db 218 FTRSNINIKVAKISMAVTLQLDTQFNCFIYCTLMYISLATNQARYPSNTATLQCLSVT 277
QY 261 IYV 263
Db 278 LHL 280

RESULT 15
Q20300 PRELIMINARY; PRT; 286 AA.
AC Q20300;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE F41H10.7 protein.
GN F41H10.7
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:26:24 ; Search time 23 Seconds
(without alignments)
653.181 Million cell updates/sec

Title: US-09-936-845a-15
Perfect score: 1545
Sequence: 1 MELAEFWNDLNTFTYGNH.....PFVKAYIIKSKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485.5	31.4	278	4	US-09-903-456-58
2	479	31.0	271	4	US-09-903-456-53
3	479	31.0	272	4	US-09-145-828A-18
4	479	31.0	272	4	US-09-903-456-24
5	476.5	30.8	261	4	US-09-903-456-60
6	435.5	28.2	265	4	US-09-903-456-64
7	360	23.3	265	4	US-09-903-456-55
8	360	23.3	265	4	US-09-903-456-89
9	360	23.3	265	4	US-09-903-456-89
10	360	23.3	265	4	US-09-903-456-56
11	327.5	21.2	238	4	US-09-903-456-62
12	327.5	21.2	238	4	US-09-145-828A-13
13	327.5	21.2	238	4	US-09-903-456-20
14	327.5	21.2	278	4	US-09-145-828A-11
15	288	18.6	141	4	US-09-903-456-18
16	280	18.1	147	4	US-09-903-456-47
17	280	18.1	147	4	US-09-145-828A-20
18	280	18.1	147	4	US-09-903-456-27
19	262	17.0	345	4	US-09-145-828A-8
20	239	15.5	276	4	US-09-903-456-15
21	239	15.5	276	4	US-09-903-456-37
22	235	15.2	272	4	US-09-149-476-415
23	233	15.1	272	4	US-09-903-456-76
24	233	15.1	272	4	US-09-903-456-75
25	233	15.1	283	4	US-09-903-456-88
26	233	15.1	288	4	US-09-903-456-84
27	233	15.1	292	4	US-09-903-456-82
28	233	15.1	295	4	US-09-903-456-86

28	232	15.0	272	4	US-09-903-456-78	Sequence 78, Appl
29	231	15.0	272	4	US-09-903-456-80	Sequence 80, Appl
30	230	14.9	272	4	US-09-903-456-79	Sequence 79, Appl
31	229	14.8	272	4	US-09-903-456-81	Sequence 81, Appl
32	226	14.6	299	4	US-09-903-456-66	Sequence 66, Appl
33	221.5	14.3	284	4	US-09-903-456-83	Sequence 83, Appl
34	221.5	14.3	292	4	US-09-903-456-35	Sequence 35, Appl
35	221.5	14.3	293	4	US-09-903-456-45	Sequence 45, Appl
36	221.5	14.3	299	4	US-09-903-456-61	Sequence 61, Appl
37	220	14.2	347	1	US-08-249-420-2	Sequence 2, Appl
38	220	14.2	347	2	US-08-737-663-2	Sequence 2, Appl
39	220	14.2	347	4	US-09-145-828A-16	Sequence 16, Appl
40	220	14.2	347	4	US-09-903-456-14	Sequence 14, Appl
41	219	14.2	283	4	US-09-903-456-85	Sequence 85, Appl
42	219	14.2	292	4	US-09-903-456-65	Sequence 65, Appl
43	216	14.0	280	4	US-09-145-828A-21	Sequence 21, Appl
44	216	14.0	280	4	US-09-903-456-28	Sequence 28, Appl
45	216	14.0	286	4	US-09-903-456-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-903-456-58
; Sequence 58, Application US/09903456
; Patent No. 6577145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58

Query Match	31.4%	Score	485.5	DB	4	Length	278
Best Local Similarity	37.7%	Pred. No.	3.3e+44				
Matches	103	Conservative	54	Mismatches	99	Indels	17
Gaps	5						
QY	23	MTTKYKSYHPPGQVADP-----QYWTILFQKYWYHSITISVLVYFLIKVIOKFMENR	76				
Db	11	VTPWYSYIFDFENFIHORTKMLENTWTF-..YVCGI-----YMLVIFGGQHFMQR	62				
QY	77	KPFTLKVLINWGLAAPSIIATLRFSDPLRSIYAGFYKTLCSY---CMPTDVAATWS	134				
Db	63	PRFQLRGFLIIWNTLLAMFSLMGAARTAPELIHLVRLHGLFHSVCVPSYIEQDRCGFWT	122				
QY	135	PAPALSKIVELGDYFILLKRPILFLHYHHAVALIYTVHSGAHTAAGFYILMNYFA	194				
Db	123	WLFVLSKLPGLDGTIFIVLRKQPLIFLHWYHHTIIVLIYSWFSYTYTSSAFAFWNYCV	182				
QY	195	FSLMYTYTVTSANGYRLPKWYSMTVTVTQTMLAGVGI-TWMYKVKYTKYKLPQQQSV	253				

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Db 183 HSMVSYALKAAFPNPRFISMIIITSLQALQMIIGCALNVWANGFLKTHGTXTSCHISOR 242
QY 254 NLXLAFVIVYTAIILOFQFVKAYIIKSKSK 286
Db 243 NNLSTAMYSYVFLPFAFFFKAYLAPGGHKS 275

RESULT 2
US-09-903-456-53
; Sequence 53, Application US/09903456
; Patent No. 6677145
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
US-09-903-456-53

Query Match 31.0%; Score 479; DB 4; Length 271;
Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLFIILIKVIOKFMENKPTTKYPLILMNGALAAFSIATLRFSDPL 108
Db 32 EBYWSSFLIVVLLIIVGQTYMTRKSPSLQRPILMSFPLAIPSLGLTRMKFWA 91
QY 109 RSLVAGFYKTLVSCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPLIFLHYHHA 167
Db 92 TWMTVGLKQVCPALYTDADVRFWSFLSKVVELGDTAFIILKRPLIFVHYHHS 151
QY 168 AVLIYTVHSGAHTAAGFYILMNYFAHSLMYTYTYSAGYRLPKVSMVTYVQTQM 227
Db 152 TVLLFTSFGYKKNKVPSCGFWMTMFGVHSMVYTYTMMKAALKHPNLLPMTVITSLQILQM 211
QY 228 LAGV-GITWVYKVKTEYKLPQOOSVANLYLAFVIVYTFALFIQFVKAYIIKSK-K 284
Db 212 VLGTIFGLNYIWR-----QKGCCHTTEHFFWFSFMLYGTIFYLFAHFFHRAYLPRPKVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 3
US-09-145-828A-18
; Sequence 18, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
US-09-145-828A-18

Query Match 31.0%; Score 479; DB 4; Length 272;
Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLFIILIKVIOKFMENKPTTKYPLILMNGALAAFSIATLRFSDPL 108
Db 32 EBYWSSFLIVVLLIIVGQTYMTRKSPSLQRPILMSFPLAIPSLGLTRMKFWA 91
QY 109 RSLVAGFYKTLVSCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPLIFLHYHHA 167
Db 92 TWMTVGLKQVCPALYTDADVRFWSFLSKVVELGDTAFIILKRPLIFVHYHHS 151
QY 168 AVLIYTVHSGAHTAAGFYILMNYFAHSLMYTYTYSAGYRLPKVSMVTYVQTQM 227
Db 152 TVLLFTSFGYKKNKVPSCGFWMTMFGVHSMVYTYTMMKAALKHPNLLPMTVITSLQILQM 211
QY 228 LAGV-GITWVYKVKTEYKLPQOOSVANLYLAFVIVYTFALFIQFVKAYIIKSK-K 284
Db 212 VLGTIFGLNYIWR-----QKGCCHTTEHFFWFSFMLYGTIFYLFAHFFHRAYLPRPKVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 4
US-09-903-456-24
; Sequence 24, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24

Query Match 31.0%; Score 479; DB 4; Length 272;
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Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYYVHSITISVLVFIILKVIQKFMENKPTLKYPLILWNGALAAAFSIIATLRFSDPL 108
Db 32 EYVWSSFLIVVYLLLVGGTYMTRKSLQRLPLWSPFLAIFSLTLRWKPKMA 91
QY 109 RSLVAGFYKTLCKSCNPTD--VAAFWSPAFALSKEVLGDTMFIILRKRPILFLHYHHA 167
Db 92 TWMTVGLKQVCFAYITDDAVREWSFLFLSKVVELGDTAFILRKRPILFVHWYHHS 151
QY 168 AVLIYVHSGAHTAAGFYILMNPYPAHSLMYTVTVSANGYRLPKWVSMVTVTOTOM 227
Db 152 TLLFTSGYKXNKVSGGFWMTNFGVHSMVTYITKAAKLGPNLPLWMTSLQILQM 211
QY 228 LAGV--GITMVMYKVKTEYKLPCCQSVANEXLAFVIYVTFAILFIQFFVKAYIIKSSK-K 284
Db 212 VIGTIFGILNIWR---QENGCHTTEHFWSEFWLYGTYPILFAHFFHRAVLRKPKVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 5
US-09-903-456-60
; Sequence 60, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2006-07-24
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; NAME/KEY: VARIANT
; LOCATION: (218)...(218)
; OTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60

Query Match 30.8%; Score 476.5; DB 4; Length 261;
Best Local Similarity 40.2%; Pred. No. 2.8e-43;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps 4;

QY 44 WTILFKYVHSTISVLVFIILKVIQKFMENKPTLKYPLILWNGALAAAFSIIATLRF 103
Db 21 WTWVP---YVCGI-----YMLVIFGQHFQMRPQLRGPLIIWTLAMFSINGAART 72
QY 104 SIDPLRLSYAEGFYKTLCSY--CNPTDVAAFWSPAFALSKEVLGDTMFIILRKRPILFL 161
Db 73 APELHVLRHYGLFHSVCVPSIEQDRVCGFTWLVLSKLPGLGDTFIVLRKQPLFL 132
QY 162 HYTHAAVLIYVHSGAHTAAGFYILMNPYPAHSLMYTVTVSANGYRLPKWVSMVTWT 221
Db 133 HWYHTITLVISYFSTYETSSARWFIWNVYCVHSMYSYALKAAAREPNPPEFSMILTS 192
QY 222 VQTQMLAGVGI--TWAVYKVKTEYKLPCCQSVANLYLAFVIYVTFAILFIQFFVKAYIIK 280
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Db 193 LQLAQMIIGCAINWANGFLKTHGTXSCHISQORNILSIAMYSYFVLFARFFYKAYLAP 252
QY 281 SSKSK 286
Db 253 GGHKS 258

RESULT 6
US-09-903-456-64
; Sequence 64, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-456-64

Query Match 28.2%; Score 435.5; DB 4; Length 265;
Best Local Similarity 35.8%; Pred. No. 7.5e-39;
Matches 95; Conservative 54; Mismatches 103; Indels 13; Gaps 5;

QY 26 KYKYSYHFPGEQVADPOYWTILFKYVHSTISVLVFIILKVIQKFMENKPTLKYPL 85
Db 10 EYFEKOFNENEAIQ---W---MOENKQSLFSAIYAAFIFGGRHLMYKRAKELRPL 63
QY 86 ILWNGALAAAFSIIATLRFSDPLRLSYAEGFYKTLCSY--YSCNPTDVAAFWSPAFALSKI 142
Db 64 VLWSLTAVFSIFCALRTGAYMVYILATKGLKQSCVCDQGFYNGP--VSKFWAYAFVLSKA 121
QY 143 VELGDTMFIILRKRPILFLHYTHAAVLIYVHSGAHTAAGFYILMNPYPAHSLMYTY 202
Db 122 PELGDTTIFILRKQKLIPLHWYHTITLVLSYWSYKDWAGGWMFTMNYGVHAWMSYI 181
QY 203 TVSAMGYRLPKWVSMVTVTQTTQMLAGVGIWAVYKVKTEYKLPCCQSVANLYLAFVIY 262
Db 182 ALRANGFVSRKFAFNTLSQITQMLMGCVNVLVFCWMOHQDQ--CHSHFQNIWFSSLMY 239
QY 263 VTFAILFIQFFVKAYTIKSSKUS 287
Db 240 LSYLVLFCHFFFEAYIGMRKTKA 264

RESULT 7
US-09-903-456-55
; Sequence 55, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
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; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-55

Query Match      23.3%; Score 360; DB 4; Length 265;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYWHSITISVLYFILIKVIOKFMENRKPFTLKYPILMNGALAAPSIATLRFSDP 107
DB 17 FADHFDVTIOASILYMWVFGTKWFMNRQPPQLTIPLINMNFILAAFSIAGAVKMTPEF 76
QY 108 LRSIYABGFYKTLCYSCNPT-DVAAFSPAFALSKIVELGDTMFIILRKRPILFLHYHH 166
DB 77 FGTIANKGIVASYCKVDFDTKGNGYWWLFWASKLFLVDITFLVLRKPLMLFLHYHH 136
QY 167 AAVLIYTVHSGAEHTAAGFYILMNYFAHSLMYTYTTSAMGYRLPKWMSMTVTVTQ 226
DB 137 ILTMIVAMYSHPITPGFNRYGIYLFVWFAFMYSYFLRSMKIRVPGFIAQAITSQIVQ 196
QY 227 MLAGVGITWMYKVKTEYKLPQOOSVANLYLAFVIYVTFALLFOFPVKAYIKSSK-KS 285
DB 197 FIISCAVLAHLGYLMHFTNANCDPSPVKLAVFMDTTTIALFVNFLOSYVLRGDKY 256
QY 286 KSV 288
DB 257 KAV 259

RESULT 9
US-09-903-456-56
; Sequence 56, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Bun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-56

Query Match      23.3%; Score 360; DB 4; Length 288;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYWHSITISVLYFILIKVIOKFMENRKPFTLKYPILMNGALAAPSIATLRFSDP 107
DB 40 FADHFDVTIOASILYMWVFGTKWFMNRQPPQLTIPLINMNFILAAFSIAGAVKMTPEF 99
QY 108 LRSIYABGFYKTLCYSCNPT-DVAAFSPAFALSKIVELGDTMFIILRKRPILFLHYHH 166
DB 100 FGTIANKGIVASYCKVDFDTKGNGYWWLFWASKLFLVDITFLVLRKPLMLFLHYHH 159
QY 167 AAVLIYTVHSGAEHTAAGFYILMNYFAHSLMYTYTTSAMGYRLPKWMSMTVTVTQ 226
DB 160 ILTMIVAMYSHPITPGFNRYGIYLFVWFAFMYSYFLRSMKIRVPGFIAQAITSQIVQ 219
QY 227 MLAGVGITWMYKVKTEYKLPQOOSVANLYLAFVIYVTFALLFOFPVKAYIKSSK-KS 285
DB 220 FIISCAVLAHLGYLMHFTNANCDPSPVKLAVFMDTTTIALFVNFLOSYVLRGDKY 279
QY 286 KSV 288
DB 280 KAV 282
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RESULT 10
US-09-903-456-62
; Sequence 62, Application US/09903456
; Patent No. 6677145
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-62

Query Match      23.3%; Score 360; DB 4; Length 288;
Best Local Similarity 31.3%; Pred. No. 1.1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FOKYVHSTISVLFIKIKVKQKFNKRPFTLKYPILMNGALAAFSIIATLRFSDP 107
DB 40 FADHDVITQASILYVGVFGTKWFRNRPQFTLPLNINWIFLAAFSAGAVKPTDF 99
QY 108 LRSLYAEGFYKTLCSNPT-DVAAPFSPAFALSKIVELGDTMFIILKRPLIFLYHH 166
DB 100 FGTIANKGIVASCKYFDFTKGENGVWVLFASKLPELVDTFLVLRKPLMFLRWYHH 159
QY 167 AAVLYTVHSGAEHTAAGFYILMNYFAHSLMYTYTVSANGYRLPKWVMTVTVTQT 226
DB 160 ILTIMYAWYSHLTPGPNRYGYLNFVHAFFMYSYPLFSKIRVPGFIAQAITSLQIVQ 219
QY 227 MLAGVGTIMWYKVKTEYKLPQOQSVAANLYLAFVIYVTFALIFQFVKAYIKSK-KS 285
DB 220 FIISCAVLAHLGYLMFTNANCDPEPSVFKLAVFMDTTLALFVNFQSVLRGCKDY 279
QY 286 KSV 288
DB 280 KAV 282

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RESULT 11
US-09-145-828A-13
; Sequence 13, Application US/09145828A
; Patent No. 6403349
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13

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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-13

Query Match      21.2%; Score 327.5; DB 4; Length 238;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91; Indels 9; Gaps 6;

QY 49 QKYVHSTISVLFIKIKVKQKFNKRPFTLKYPILMNGALAAFSIIAT---LRFSI 105
DB 20 QEHFGLFVQMAIAYVILVFSIKRFRDREPQLTALTALRNWFFLSVFSYGSWTWFFPMV 79
QY 106 DPLRSLYAEGFYKTLCSY-CNPTDVAAPFSPAFALSKIVELGDTMFIILKRPLIFLYHH 164
DB 80 QQIR-LY--GLYGCCEALSPLPSQAEYWLFTLILSKAVFVDFVDFLVRKPKLIFLHWY 136
QY 165 HAAVLYTVHSGAEHTAAGFYILMNYFAHSLMYTYTVSANGYRLPKWVMTVTVTQT 224
DB 137 HMAITVFFCSNYPTPSSQSRVGVINLVFHAFFMYPYFTFSMNKIKVPAKISMAVTVLQL 196
QY 225 TOMLAGV-GITWYKVKTK-BYKLPQOQSVAANLYLAFVIYV 263
DB 197 TQFMCFIYGCTLMYSLATNOARYPSNTPATLQCLSLTYLHL 237

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RESULT 12
US-09-903-456-20
; Sequence 20, Application US/09903456
; Patent No. 6677145
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-20

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Query Match      21.2%; Score 327.5; DB 4; Length 238;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91; Indels 9; Gaps 6;

QY 49 QKYVHSTISVLFIKIKVKQKFNKRPFTLKYPILMNGALAAFSIIAT---LRFSI 105
DB 20 QEHFGLFVQMAIAYVILVFSIKRFRDREPQLTALTALRNWFFLSVFSYGSWTWFFPMV 79
QY 106 DPLRSLYAEGFYKTLCSY-CNPTDVAAPFSPAFALSKIVELGDTMFIILKRPLIFLYHH 164
DB 80 QQIR-LY--GLYGCCEALSPLPSQAEYWLFTLILSKAVFVDFVDFLVRKPKLIFLHWY 136
QY 165 HAAVLYTVHSGAEHTAAGFYILMNYFAHSLMYTYTVSANGYRLPKWVMTVTVTQT 224
DB 137 HMAITVFFCSNYPTPSSQSRVGVINLVFHAFFMYPYFTFSMNKIKVPAKISMAVTVLQL 196
QY 225 TOMLAGV-GITWYKVKTK-BYKLPQOQSVAANLYLAFVIYV 263
DB 197 TQFMCFIYGCTLMYSLATNOARYPSNTPATLQCLSLTYLHL 237

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RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      21.2%; Score 327.5; DB 4; Length 278;
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels 11; Gaps 6;

QY 55 SITISVLVFLIKVIOKFNENKPTLKYPLILNWCALAAFSIATLRSIDPLRS-LYA 113
Db 30 SAKLAVGIATIPGLKYMKDKRKAFLDSTPLNINWILSTFSLGFL-FTFPTLLSVIRK 88
QY 114 EGFYKTLCY--SCNPTDVAAPFSPALSKIVELGDTMFIILKRPFLIFLHYHAAVLI 171
Db 89 DGFSTYSHVSELYTDSGTGYWIFLWISKIPELLDTVFLVLRKRPFLIFEMWYHATGY 148
QY 172 YTV---HSGAHTAGRFILMYFAHSLMYTYTYSANGYRLPKWVMTVTVTOTML 228
Db 149 YALVCYHEDAVHMV---WVWMNYIIHAFMYGYLLSKLKVPIPPSVAQAITSQMVQFA 205
QY 229 AGV-GITMVMYKVKTEYKLPQQQSVANLYLAFVIYVTFAILFIQFVKAYIIKSKSKKS 287
Db 206 VAIFAQVHSYKHVYEGVEGLAYSFRGTAIGFMTTYFYLWIQFYKHYLNGGKKYNL 265
QY 288 VKNE 291
Db 266 AKDQ 269

RESULT 14
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (141)...(141)
; OTHER INFORMATION: Xaa = Unknown or Other at position 141
US-09-903-456-18

Query Match      18.6%; Score 288; DB 4; Length 141;
Best Local Similarity 39.0%; Pred. No. 2.5e-23;
Matches 55; Conservative 36; Mismatches 48; Indels 2; Gaps 1;

QY 147 DTMFIILKRPFLIFLHYHAAVLIYTVHSGAHTAGRFILMYFAHSLMYTYTUSA 206
Db 1 DTPIILKOKKLIPLHWYHITVLLYSWYSYKDKVAGCGWMTWYGVHVMYSYALRA 60
QY 207 MGYELPKWVMTVTVTOTMLAGVITMVKYKVKTEYKLPQQQSVANLYLAFVIYVTF 266
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; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      21.2%; Score 327.5; DB 4; Length 278;
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels 11; Gaps 6;

QY 55 SITISVLVFLIKVIOKFNENKPTLKYPLILNWCALAAFSIATLRSIDPLRS-LYA 113
Db 30 SAKLAVGIATIPGLKYMKDKRKAFLDSTPLNINWILSTFSLGFL-FTFPTLLSVIRK 88
QY 114 EGFYKTLCY--SCNPTDVAAPFSPALSKIVELGDTMFIILKRPFLIFLHYHAAVLI 171
Db 89 DGFSTYSHVSELYTDSGTGYWIFLWISKIPELLDTVFLVLRKRPFLIFEMWYHATGY 148
QY 172 YTV---HSGAHTAGRFILMYFAHSLMYTYTYSANGYRLPKWVMTVTVTOTML 228
Db 149 YALVCYHEDAVHMV---WVWMNYIIHAFMYGYLLSKLKVPIPPSVAQAITSQMVQFA 205
QY 229 AGV-GITMVMYKVKTEYKLPQQQSVANLYLAFVIYVTFAILFIQFVKAYIIKSKSKKS 287
Db 206 VAIFAQVHSYKHVYEGVEGLAYSFRGTAIGFMTTYFYLWIQFYKHYLNGGKKYNL 265
QY 288 VKNE 291
Db 266 AKDQ 269

RESULT 15
US-09-903-456-47
; Sequence 47, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (141)...(141)
; OTHER INFORMATION: Xaa = Unknown or Other at position 141
US-09-903-456-47

Query Match      18.6%; Score 288; DB 4; Length 141;
Best Local Similarity 39.0%; Pred. No. 2.5e-23;
Matches 55; Conservative 36; Mismatches 48; Indels 2; Gaps 1;

QY 147 DTMFIILKRPFLIFLHYHAAVLIYTVHSGAHTAGRFILMYFAHSLMYTYTUSA 206
Db 1 DTPIILKOKKLIPLHWYHITVLLYSWYSYKDKVAGCGWMTWYGVHVMYSYALRA 60
QY 207 MGYELPKWVMTVTVTOTMLAGVITMVKYKVKTEYKLPQQQSVANLYLAFVIYVTF 266
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Db 61 AGFRVSRKFAPIITLSQITQMLMGCVVNYLVFCWQHDO-CHSHFQNIWFSSSLMYLSYL 118
QY 267 ILFIQPFVXAYILKSSKKS 287
Db 119 VLFCHFFFEAYIGMRKTKA 139

Search completed: June 16, 2004, 15:30:08
Job time : 24 secs